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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 18, 2005, 15:03:42; Search time 169 Seconds (without alignments) 1096.202 Million cell updates/sec

Title: Perfect score:

2500 1 MDATIAPHRIPPEMPQYGEE.....YTVPEY1ESGIINPLPKKIP 479 US-10-798-773-2

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*
11: geneseqp1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	Abb82701	Ada55452	Aae34860	Adc10110	Adc10108	Aam38895	Aae16279	Adb65473	Aae07843	Abw00581	Aam40681	Aau17305	Adb94013	Aam78417	Aam79401	Abq59945	Aau17614	Aau17303	Aam85250	Adb94322	Adb94011	Abb82702	Abb93735	Adn74247	Abu44285
SUMMARIES	£	91	ABB82701	ADA55452	AAE34860	ADC10110	ADC10108	AAM38895	AAE16279	ADB65473	PAE07843	ABW00581	AAM40681	AAU17305	ADB94013	AAM78417	AAM79401	ABG59945	AAU17614	4AU17303	AAM85250	ADB94322	ADB94011	ABB82702	ABB93735	ADN74247	ABU44285
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ALIGNMENTS

RESULT 1 ABB82701 ID ABB82701 standard; protein; 479 AA.	XX AC ABB82701;	DT 07-MAR-2003 (first entry)	DE NOvel human kinase polypeptide (NHP).	XX NHP; kinase; gene therapy; drug screening; hu XX	OS Homo sapiens.	AA WO200290517-A2.	14-NOV-2002.	PF 08-MAY-2002; 2002WO-US014669.	AX PR 09-MAY-2001; 2001US-0289727P.	PA (LEXI-) LEXICON GENETICS INC. XX	I Yu X, Xie Q, Abuin A, Walke DW;	R WPI; 2003-103514/09. R N-PSDB; ABV75301.	New human kinase proteins and polynucleotid nutriceutical applications, drug screening,	diagnosing or treating diseases imbalances.	A S Claim 3; Page 38-39; 40pp; English. X	The invention relates to novel human polypep	activity and polynucleotides end proteins, antibodies, agonists		The proteins and polynucleotides	applications, for identifying protein coding unique gene to a particular chromosome. The s	polynucleotides and proteins can also be use	bio]	
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uman; enzyme.

09-MAY-2001; 2001US-0289727P. 08-MAY-2002; 2002WO-US014669. 14-NOV-2002.

New human kinase proteins and polynucleotides, useful for cosmetic and nutriceutical applications, drug screening, clinical trial monitoring, diagnosing or treating diseases associated with biological disorders or imbalances.

The invention relates to novel human polypeptides (NHP) having kinase activity and polynucleotides encoding them. The polynucleotides, proteins are useful for drug screening, clinical trial monitoring, and diagnosing or treating diseases or disorders associated with biological disorders or imbalances. The proteins and polynucleotides are useful in comestic and nurricentical applications, for identifying protein coding sequences and mapping a unique gene to a particular chromosome. The sequence of the polynucleotides and proteins can also be used as additional DNA markers for restriction fragment length polymorphism analysis, or in forensic biology. The present sequence represents a NHP kinase

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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
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                                            1 MDATIAPHRIPPEMPQYGEENHIFELMQNMLEQLLIHQPEDPIPFMIQHLHRDNDNVPRI
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                479;
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24-JAN-2002; 2002US-0350435P.
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Seki N, Yoshikawa T,
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N-PSDB; ADA53813.
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
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                                                                                                                                  The present invention relates to novel human secretory or membrane proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS4031-ADAS4071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                               Claim 14; SEQ ID NO 3020; 205pp; English
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                                                                            421 NPKDAEEQVKLKMDLFYRNSADLEQLYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
                                                                                                421 NPKDAEEQVKLKMDLFYRNSADLEQLYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
361 QAHLLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPFTMEIQARLLL
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04-JUN-2001, 2001US-0295601P.
06-JUN-2001, 2001US-0295418P.
06-JUN-2001, 2001US-0295418P.
11-JUN-2001, 2001US-0295418P.
12-JUN-2001, 2001US-0295573P.
12-JUN-2001, 2001US-0297567P.
14-JUN-2001, 2001US-0297567P.
15-JUN-2001, 2001US-0297567P.
19-JUN-2001, 2001US-029756P.
19-JUN-2001, 2001US-029958P.
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23-JUN-2001, 2001US-030989P.
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28-JUN-2001, 2001US-031456P.
28-JUN-2002, 2002US-035993F.
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                                                                                                                                                                                                                                                                                                                               Yue H, Lu DAM, Azimzai Y, Ding L, Lee EA, Hafalia AJA, Becha SD; Tang YT, Lal PG, Griffin JA, Gururajan R, Ramkumar J, Ellott VS; Arvizu CS, Luo W, Swarnakar A, Duggan BM, Tran UK, Walia NK, Gandhi AR, Yao MG, Khan FA, Baughn MR, Borowsky ML, Zebarjadian Y Richardson TW, Marquis JP, Chien D, Jin P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPQTGEIXHTTFDWPPESEIQNRLMVPEDISELETAQKLLEYHRNIVRVIPSYPKILKVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Col 133-134; 82pp; English.
                                                                                                         24-MAY-2001; 2001US-0293665P.
15-UTN-2001; 2001US-0298712P.
05-UTL-2001; 2001US-0303418P.
27-UTL-2001; 2001US-0306967P.
27-UTL-2001; 2001US-0308183P.
19-DEC-2001; 2001US-0343007P.
15-FEB-2002; 2002US-0357675P.
                                                                          23-MAY-2002; 2002WO-US016634
                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 479; Conservative
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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obseity, and andocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWVLHGVPRDLDQAHLLARLGYNPNRVFFLANVPFDSIMERLTLRRIDPVTGERYHLMYKP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HIHRDNDNVPRIVILGPPASGKTITAMMLCKHLNSSLITLENLILNEFSYTATEARRIXL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQKYRLVINVCCGQLLXEAVADRTTFGELIQPFFEKEMAVPDSLLMKVLSQRLDQQDCIQK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPIMEIQARLLQNPKDAEEQVKLKMDLFYRNSADLEQLYGSAITLNGDQDPYTVFEYIES 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLHRDNDNVPRIVILGPPASGKTTIAMWLCKHLNSSLLTLENLILNEFSYTATEARRLYL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRKTVPSALLVQLIQERLABEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVLIERNIGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLLEYHRNIVR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA; Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda I Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I; Ort T, Paddigaru M, Patturajan M, Pena CEA, Rafeelli L, Rieger DK; Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK; Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP; Burgess CE, Lepley DM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 99.4%; Score 2484; DB 7; Length 491; al Similarity 97.6%; Pred. No. 1.9e-232; 479; Conservative 0; Mismatches 0; Indels 12
                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 130; 772pp; English.
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N-PSDB; ADC10109.
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cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antidiammatory; gene therapy; antisenspy; thyrominetic; NOVX; pathology; cancer; diabetes; obseity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipippo VA, Edinger SR, Eisen A, Ellerman K, GangOlli EA;
Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda F
Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkers RA, Smithson G, Spaderna SK;
Spytek RA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
                                                                                                                                                                         Human NOVX polypeptide SEQ ID NO: 128
                            ADC10108 standard; protein; 510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-0295601P

2001US-02956410P

2001US-0296410P

2001US-0296410P

2001US-0296575P

2001US-0295573P

2001US-0295573P

2001US-029523P

2001US-029523P

2001US-0299133P

2001US-0299133P

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2001US-039133P

2001US-039133P

2001US-039133P

2001US-039133P

2001US-039132P

2001US-030153P

2001US-035913P

2002US-035913P

2002US-035913P
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                                                                                                                          entry)
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Lepley DM;
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                                                                                                                                                                                                                                                                                                                             predictive medicine.
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N-PSDB; ADC10107.
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12 - JUN - 2001)
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18 - JUN - 2001)
21 - JUN - 2001)
22 - JUN - 2001)
28 - JUN - 2001)
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25-SEP-2001;
03-DEC-2001;
14-DEC-2001;
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21-FEB-2002;
22-FEB-2002;
22-FEB-2002;
22-FEB-2002;
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11-JUN-2001;
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Burgess CE,
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                                                                                           The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The Novx polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, disbetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the
                                                                                                                                                                                                                                                                                                                                135
                                                                                                                                                                                                                                                                                                                                                        VILGPPASGKTTIAMWLCKHLNSSLLTLENLILNEFSYTATEARRLYLORKTVPSALLVO 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 QAHLLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 QAHLIARLGYNPNRVFFLAVPPEDSIMERLTLERRIDPVTGERYHLAYKPPPTWEIQARLLQ 451
           New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPKDAEEQVKLKMDLFYRNSADLEQLYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
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                                                                                                                                                                                                                                                                                                                     1 MDATIAPHRIPPEMPQYGEENHIFELMQNWLEQLLIHQPEDPIPFMIQHLHRDNDNVPRI
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                                                                                                                                                                                                                                                                              0; Indels 44; Gaps
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                                                                      Claim 1; SEQ ID NO 128; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 2040.
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                                                                                                                                                                                                                                                                  Local Similarity 90.8
hes 435; Conservative
                                                                                                                                                                                                                              Sequence 510 AA;
                                              CNS diseases.
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAAI8642-AAM46213) with noctropic.

Cocoded polypeptides (AAAI8642-AAM46213) with noctropic.

Immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous for alread neuropathies and central nervous system disease, anyotrophic lateral sclerosis, and shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukeemias and control specification chis patent did not form by the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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, Zhao Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 LIQERLAEEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVLIERNLGKRI
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Zhang J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.8%; Score 1571; DB 4; Length 571;
llarity 53.6%; Pred. No. 1.9e-143;
Conservative 4; Mismatches II; Indels 276
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Yang Y,
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Έ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                   21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552117.
20-UDN-2000; 2000US-00598042.
19-JUL-2000; 2000US-005312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-0065311.
19-CT-2000; 2000US-006391.
29-NOV-2000; 2000US-0063934.
                                                                                                         26-DEC-2000; 2000WO-US034263
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WO200153312-A1
                                                                                                                                                              23-DEC-1999;
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Best Local Si
Matches 336,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J,
Zhou P,
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Human; kinase; PKIN-25; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crobn's disease; Hodgkin's disease; adquired Immune Deficiency Syndrome; ALDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis; odo pasture is syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy.
                                                                                                                                                                                                                                                                                     436 QGPQEKEKQMPASPMNTDAHLDINFKEGLKKERSYTGQFEANVRDEERQCGCGVVPDSLL 495
                                                                                   QLLKEAVADRITFGELIQPFFEKEMAEGGHRVKGTVEFSFRTLPCNQKDLPCLLKLEDML 315
                                                                                                                                                                                        326
                                                                                                                                                                                                                         376 DIGSFSLGCERGLQRQGQDWRGEEEVAPVTLCSLYTYDQGDSLDLLGPIGILQEGRDPGT 435
                                                                                                                                                                                                                                                                                                                        MKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDSIMERLTLR 392
316 LYPLRLSELPEEELLVGALPYTFGESLETSQIPLFNPRPPNGRCSLKPLSLWEHPRLTGA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT; Bughn. MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
                                                                                                                                                                                                                                                                                                                                             QLLKEAVADRTTFGELIQPFFEKEMA------
                                                                                                                                                                                                                                                                                                                                                                                          393 RIDPVTGERYHLMYKPPPTMEIQARLL 419
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30-JJN-2000; 2000US-0215651P.
07-JJL-2000; 2000US-0216605P.
13-JJL-2000; 2000US-0218372P.
25-AUG-2000; 2000US-0228056P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human kinase PKIN-25 protein.
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The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, Impubnoma, melanoma, allergies, adult respiratory distress syndrome, attorimume thyroiditis, gout, bronchitis, Crohn's disease, diabetes autoimume thyroiditis, gout, bronchitis, Crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, creating syndrome, uveitis, ulcerative colitis, osteoporosis, pancreatitis, potozoals and helminthic infections; bacterial, parasitic, fungal, viral, protozoal and helminthic infections; crowth and development disorders (arteriosclerosis, cirrhosis, hepatitis, crohing's syndrome, typothyroidism, cerebral palsy, cataracts); cardio croscular disease (arteriovenous fistula, hypertension, vaculitis, crohing sease, chronic bronchitis, lung tumours); lipid disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, chronic broncherent sequence is human protosi.
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                                                                        New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein encoded by clone TESTI20244460.
                                                                                                                                                                   Claim 1; Page 173-174; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB65473 standard; protein; 275 AA.
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               WPI; 2002-090207/12.
N-PSDB; AAD26472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 275 AA;
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ID ADB6
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AC ADB6
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DT 04-1
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DE Huma
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KW Huma
KW Cell
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel CC from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide for the polynucleotide, immunologically sessiving the polypeptide or peptide of the polynucleotide, immunologically sessiving the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide of the polynucleotide by contacting the polynucleotide or peptide of the matribody of the encoded protein, and observing the binding contacting the two, a transformant carrying the polynucleotide in an expressible manner and a antistance polynucleotide. The oilgonucleotide captures to expressible manner and an antistance polynucleotide. The oilgonucleotide of the secreting the polynucleotide. The polynucleotide and encoded gene may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a probe of gene therapy. The genes are involved in tissue and/or cell a transcription-related proteins, signal transduction-related proteins, centering them can be used as indicators for diseases (e.g. osteoporosis, centrological diseases, cancer, tumours. The CDNA may be used to regulate to the activity or expression of the encoded protein to treat diseases. The copy expression of the menced as indicators for diseases (e.g. osteoporosis, centrological diseases, cancer, tumours. The CDNA may be used to regulate the encoded protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed general partern of the sequence information supplied by the contact of the copy of the copy of the procession of the sequence information supplied by the
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Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 APFTPRVLLIGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGGELIQPFFEKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
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  transcription-related protein; osteoporosis; neurological disease;
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100.0%; Pred. No. 4.2e-130;
tive 0; Mismatches 0;
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(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 222pp; English.
                                                                                                                                                                                               28-MAR-2002; 2002EP-00007401.
                                                                                                                                                                                                                                          05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275; Conservative
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European Patent Office.
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N-PSDB; ADB63503.
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Best Local Similarity
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                                                                 Homo sapiens.
                                                                                                         EP1308459-A2
                                                                                                                                                    07-MAY-2003.
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385 IMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQNPKDAEEQVKLKMDLFYRNSADLE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New adenylate kinase polypeptide for diagnosing/treating cellular proliferative and/or differentiative, neurological, immune, inflammatory, lymphatic, cardiovascular, respiratory and hematological disorders.
                                                                                                                                                                                                                                                                                                                                                             Human; 27802 protein; adenylate kinase; cellular proliferative disorder; neurological disorder; inflammatory disorder; hymphatic disorder; cardiovascular disorder; inflammatory disorder; haematological disorder; cardiovascular disorder; perpiratory disorder; haematological disorder; crohn's disease; atherosclerosis; pernicious anaemia; asthma; leukaemia; acquired immune deficiency syndrome; NBS; multiple sclerosis; lymphoma; Alzheamer's disease, systemic lupus erythematosus; SLB; gene therapy; lymphoblastic leukaemia; T-cell neoplasm; cytostatic; neuroprotective; tissue typing; antiarterioslerotic; chromosomal mapping; nootropic; dermatological; antiinflammatory; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present amino acid sequence is human 27802 adenylate kinase. The 27802 protein and its corresponding nucleotide sequence is useful for modulating, disgnosing and treating cellular proliferative and/or differentiative, neurological, inflammatory, lymphatic, cardiovascular, immune, respiratory and haematological disorders. 27802 sequence is useful for treating immune disorders (e.g., crohn's disease), disorders involving blood vessels (e.g., atherosclerosis), disorders involving red cells (e.g., pernicious anaemia), respiratory disorders involving red disorders involving brain and lymph nodes (e.g. acquired immune disorders shoolving brain and lymph nodes (e.g. acquired immune deficiency syndrome (AIDS), multiple sclerosis, Alzheimer's disease), disorders involving T-cells (e.g., systemic lupus erythematosus),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Human mature 27802 adenylate kinase"
201. .251
/note= "Adenylate kinase domain 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Adenylate kinase domain 1"
                                                                                                 241 QLYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 275
                                                                           QLYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .56
'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                           AAE07843 standard; protein; 258 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chun M;
                                                                                                                                                                                                                                                                                                                            Human 27802 adenylate kinase.
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                                                                                                                                                                                                                                                                                     (first entry)
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/note= "Ac
57. .258
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N-PSDB; AAD14324.
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                                                                                                                                                                                                                                                  AAE07843;
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diseases involving haematopoietic stem cells (e.g., leukaemia), disorders involving B-cells (e.g., lymphoblastic leukaemia/lymphoma) and disorders involving precursor T-cell neoplasms. 27802 sequence is useful for modulating cellular growth and/or cellular metabolic pathways, particularly for regulating one or more proteins involved in growth and metabolism. 27802 DNA is used in gene therapy. 27802 sequence or its antibody are useful in screening assays, detection assays (e.g., chromosomal mapping, tissue typing, forensic biology), preventive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics) and in methods of treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTYVQSNHRTNAPFTPRVLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTT 312
                                                                                                                                                                                                                                                                                                                                                         KQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVLIERNLGKRIDPQTGEIYHTTF 192
                                                                                                                                                                                                                                                                                                                                                                                                                            DWPPESEIQNRLMVPEDISELETAQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQ 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ATPase-like protein; phosphatidyleerine synthase-like protein; DNA fragmentation factor-like protein; vesicle-mediated transport; phospholipid scramblase-like protein; adenylate kinase protein; organelle biogenesis; cell-cycle requlation; primary brain lymphoma; protein degradation; splenomegaly; pulmonary embolism; Hodgkin disease; atresia; tuberculosis; astrocyte; apoptosis; neurodegenerative disease; DNA fragmentation; autoimmune disorder; cancer; blood clotting system; immune system; haematopoietic; hypertension; systemic sclerosis; leukopaenia; oligodendrocyte; enzyme.
                                                                                                                                                                                                                                                                                                           61 KQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVLIERNLGKRIDPQTGEIYHTTF
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/note= "Casein kinase II (CK2) phosphorylation site"
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    .30
    /note= "Casein kinase II (CK2) phosphorylation site"

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                                                                                                                                                                                                                       52.0%; Score 1301; DB 4; Length 258; 99.6%; Pred. No. 1.1e-117; ive 1; Mismatches 0; Indels (
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/note= "Domain 1"
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/note= "N
                                                                                                                                                                                                                                          al Similarity 99.6
253; Conservative
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                                                                                                                                                                                          Sequence 258 AA;
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Best Local &
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Matches
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activity such as splenomegaly, pulmonary embolism, arrests and primary brain lymphoma. The human phosphatidylserine synthase-like molecules are useful for modulating the biosynthetic pathway involving the synthesis of the membrane phosphatidylserine (FS). They human phosphatidylserine synthase-like molecules are useful for treating disorders associated with aberrant human phosphatidylserine synthase activity such as tuberculosis, astrocytes and Hodgkin disease. The human 5698, MDA fragmentation factor-like molecules are useful for modulating apoptotic events, including DNA fragmentation. The human 5698 molecules are useful for treating diseases such as autoimmune disorders, neurodegenerative diseases and cancer. The

human 32621, phospholipid scramblase-like modecules are useful for modulating immune, haematopoietic and blood clotting systems. They are useful for treating a disorder associated with aberman human phospholipid scramblase-like protein activity such as leukopaenia and systemic sclerosis. The human 27802 adenylate kinase are useful for modulating cellular growth and/or cellular metabolic pathways. They are

proteins, phosphatidylserine synthase-like proteins, DNA fragmentation factor-like proteins, phospholipid scramblase-like proteins or adenylate kinase proteins and polynucleotides encoding such proteins. The human Arpase-like molecules are useful for modulating Arpase function. They are useful in modulating organelle biogenesis, cell-cycle regulation, protein degradation and vesicle-mediated transport. They are also useful for transing disorders associated with aberrant Arpase-like expression or treating disorders associated with aberrant Arpase-like expression or treating disorders associated with aberrant Arpase-like expression or treating disorders.

present invention relates to novel proteins including ATPase-like

Claim 8; Fig 28; Opp; English.

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New isolated polypeptides including phosphatidylserine synthase-like polypeptide useful for identifying a compound which binds and modulates activity of the polypeptide useful for treating diseases, e.g. cancer.
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                                          118. .121
/note= "Casein kinase II (CK2) phosphorylation site"
139. .142
                                                                                                                (CK2) phosphorylation
                                                                                                                                                             "Protein kinase C (PKC) phosphorylation
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                                                                                                                                                                                                                                                            'note= "ATP/GTP binding site motif"
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                                                                                                                "Casein kinase II
                    note= "Amidation site"
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2000US-0185609P.
2000US-0185946P.
2000US-0185947P.
2000US-0186234P.
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21-FEB-2001; 2001US-00790179.
21-FEB-2001; 2001US-00790180.
22-FEB-2001; 2001US-00790838.
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                                                                                                                /note=
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Modified-site
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29-FEB-2000;
29-FEB-2000;
                                             Modified-site
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12-FEB-2001;
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useful for treating hypertension, atherosclerosis and oligodendrocytes. The present sequence is human 27802, adenylate kinase protein
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                                                                                                                                            61 KQGWILDGIPETREQALRIQTIGITPRHVIVLSAPDTVLIERNIGKRIDPQTGEIYHTTF
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J, Zhao (
                                                                                                        KOGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVLIERNLGKRIDPQTGEIYHTTF
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Zhang J,
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                                                 Length 258;
                                                                     0; Indels
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Yang Y,
                                                Query Match 52.0%; Score 1301; DB 7;
Best Local Similarity 99.6%; Pred. No. 1.1e-117;
Matches 253; Conservative 1; Mismatches 0;
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Xue AJ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                              AAM40681 standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 5612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1999) 99US-00471275.
21-7AR-2000; 2000US-00486725.
25-ARR-2000; 2000US-00552317.
20-UTN-2000; 2000US-0058042.
19-UUL-2000; 2000US-00650312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-0065311.
19-CCT-2000; 2000US-0065313.
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N-PSDB; AAI59837.
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                              Sequence 258 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia.
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Wang J, 1
Zhou P, 0
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAMS1642-AAM4213) with noctropic,

concoded polypeptides (AAMS1642-AAM4213) with noctropic,

immunosuppressant and cytostatic activity. The polynuclectides are useful

continuous in the invention may be used to treat diseases of the peripheral nervous

system, such as peripheral nervous injuries, peripheral nervous

containsed neuropathies and central nervous system diseases, such as

localised neuropathies and central nervous system diseases, such as

altheimer's, Parkinson's disease, Huntington's disease, amyotrophic

lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

utilisation of the activities such as: Immune system suppression,

activin/inhibin activity, chemoteactic/chemotante cativity, haemostatic

and thrombolytic activity, ancer diagnosis and therapy, drug screening,

assays for receptor activity, arthritis and inflammation, leukaemias and

contained specification

part of the printed specification
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDATIAPHRIPPEMPQYGEENHIFELMQNMLEQLLIHQPEDPIPFMIQHLHRDNDNVPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 MDATIAPHRIPPEMPQYGEENHIFELMQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.4%; Score 1184.5; DB 4; Length 240; Best Local Similarity 83.9%; Pred. No. 2.2e-106; Matches 234; Conservative 0; Mismatches 0; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel signal transduction pathway protein, Seq ID 870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SADQPCVDVFYQALTYVQSNHRTNAPFTPRVLLLGPVGS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SADQPCVDVFYQALTYVQSNHRTNAPFTPRVLLLGPVGS
                                                                                    Example 2; SEQ ID NO 5612; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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WO200154733-A1. Homo sapiens

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Ruben SM
                                                                                                                         2000US-0237039P.
2000US-0237039P.
2000US-0239937P.
2000US-0241785P.
2000US-0241785P.
2000US-0241809P.
2000US-0241809P.
2000US-0241809P.
2000US-0246474P.
2000US-0246524P.
2000US-0246214P.
2000US-0249214P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC,
29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-SEP-2000; 20-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-2001;
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   X
                                                                                       31-JAN-2000) 2000US-0119065P.

24-FEB-2000) 2000US-0118654P.

02-MAR-2000) 2000US-0118656P.

16-MAR-2000) 2000US-0118656P.

16-MAR-2000) 2000US-01189814P.

11-MAY-2000) 2000US-01189814P.

11-MAY-2000) 2000US-0119817P.

11-JUL-2000) 2000US-0211880P.

11-JUL-2000) 2000US-0211880P.

11-JUL-2000) 2000US-0211880P.

11-JUL-2000) 2000US-0211880P.

11-JUL-2000) 2000US-021189P.

11-JUL-2000) 2000US-021189P.

11-JUL-2000) 2000US-021189P.

11-JUL-2000) 2000US-02118P.

11-JUL-2000) 2000US-02218P.

11-JUL-2000) 200US-02218P.

11-JUL-2000 2
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                                                          17-JAN-2001; 2001WO-US001312
                      02-AUG-2001
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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a
           The invention relates to novel isolated polypeptides (I), and diagnosing preventing and treating diseases including immune system diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sicke cell anaemia), myeloproliferative diseases. (e.g. squcher's disease and cancer), neurodegenerative disorders (e.g. disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. disorders (e.g. disease), chromosomal abnormalities (e.g. disorders disease, Parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. olowerulonephritis), cardiovascular disorders (e.g. arrhychmia), respiratory disorders, dematological disorders (e.g. Alzimanial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders (isorders (e.g. Addison's childnamatory disorders), liver disorders (distrabasis), as simulators of disease), reproductive system disorders, in wound healing, childnamatory disorders, liver disorders (distrabasis), as simulators of the machine affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AlbS). Addison's sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEDISELETAQKILEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQSNHRTNAP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PEDISELETAQKILEYHRNIVRVIPSYPKILKVISADQPCYDVFYQALTYVQSNHRTNAP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human, autoimmune disease, Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; immunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTPRVLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptides useful for diagnosing, treating, preventing and/or. prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 QALRIQTIGITPRHVIVLSAPDTVLIERNIGKRIDPQTGEIYHTTFDWPPESEIQNRLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.6%; Score 1166; DB 4; Length 236; Best Local Similarity 100.0%; Pred. No. 1.4e-104; Matches 225; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 870; 880pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB94013 standard; protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003 · (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel protein #247.
WPI; 2001-465460/50.
N-PSDB; AAS27222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002168711-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
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New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC;
                                                                                                                                                                                                                                                                                                                                                          2000US-0229247P
2000US-0229247P
2000US-0229344P
2000US-0229344P
2000US-0229344P
2000US-0229313P
2000US-023913P
2000US-023913P
2000US-023913P
2000US-023913P
2000US-023913P
2000US-023427P
2000US-023423P
2000US-023423P
2000US-023423P
                              17-JAN-2001; 2001US-00764868.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADB93390
                                                                                                                                                                                                                                                             14-MG-2000,
14-MG-2000,
14-MG-2000,
14-MG-2000,
14-MG-2000,
30-MG-2000,
30-MG-2000,
01-SEP-2000,
01-SEP-2000,
01-SEP-2000,
01-SEP-2000,
01-SEP-2000,
01-SEP-2000,
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02-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
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29-SEP-2000;
29-SEP-2000;
14-NOV-2002
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2000US-00560875. 2000US-00620325

27-APR-2000; 20-JUN-2000; 19-JUL-2000;

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pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the perpeptide. The polypeptide is also useful for identifying a binding partner and determining whether the binding pattner and clerk is useful for preventing, treating, or amaliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid polypeptide or the nucleic acid to a pathological condition or susceptibility to a pathological condition or susceptibility, thrombocytopenia. The polypeptide, the nucleic acid and the antibody are useful as immunosuppressive agents, the nucleic acid and the antibody are useful as immunosuppressive agents, affinity antibodies and increase serum immunosuppressive agents.

Or season sequence represents the amino acid sequence of a novel human caffinity antibodies and increase serum immunosuppressive of the manner of present esquence data for this patent did not form part of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 236 AA;
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266
                                                                                                               147 QALRIQILGITPRHVIVLSAPDTVLIERNIGKRIDPQIGEIYHTTPDWPPESEIQNRLMV 206
                                                                                                                                                 FTERVILLGEVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMA 326
                                                                                                                                                               9
                                                              207 PEDISELETAQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQSNHRTNAP
                           ö
46.6%; Score 1166; DB 7; Length 236; 100.0%; Pred. No. 1.4e-104; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                 VPDSILMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYN 371
                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 225; Conservative
                                                                                                                                                     267
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AAM78417 standard; protein; 248 Human protein SEQ ID NO 1079. (first entry) 06-NOV-2001 AAM78417;

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.

Homo sapiens

WO200157190-A2

05-FEB-2001; 2001WO-US004098

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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell propulations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activities activity, tissue growth factor activity, immunomodulatory activity and activity, infinity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system diagnosis and/or treatment of cancer, leuksemia, nervous system diagnosis, arthritis and inflammation. Note: Records for SBO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 VPDSLIMKVLSQRLDQQDCIQKGWVLHGVERDLDQAHLLNRLGYNPNRVFFLNVPFDSIM 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 VPDSLLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDSIM 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215
                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                            Cao Y;
R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 ERLTLRRIDPVTGERYHLMYKPPTWEIQARLLQNPKDAEEQVKLKMDLFYRNSADLEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 248;
                                                                                                                                                                                              xu C, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                              Asundi V, Zhou P, X
J, Zhang J, Ren F,
Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
32.2%; Score 806; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 1.6e-69;
Matches 153; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 YGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 YGSAITLNGDQDPYTVFEYIESGIINPLPKKIP
                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 3307; 6221pp; English.
                                                                                                                                                                                                                   Wang D, Wang
Wejhrman T,
                                                                                                                                                                                                  Drmanac RT,
                                                                                                                                                                                                                                                                                                                                               in diagnosis and gene therapy
                                                                01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                                                                                                                                         WPI; 2001-476283/51.
                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                              Tang YT, Liu C,
Ma Y, Zhao QA,
Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 248 AA;
                                                                                                                                                                                                                                                                                            N-PSDB; AAK51550
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AAM79401 standard; protein; 226 AA Human protein SEQ ID NO 3047. 06-NOV-2001 (first entry) AAM79401; 5×5×5×5×5×5×5×5×

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.

Homo sapiens

WO200157190-A2.

```
The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymoleotides and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, hematopolesis regulating activity, tissue growth factor activity, hematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and crowinishin activity and may be useful in the disponsis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 237; 6221pp; English.
                                                                                                                                                                       20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-0062032.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065361.
20-OCT-2000; 2000US-00693125.
30-NOV-2000; 2000US-0073422.
                                                                                      05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-476283/51.
N-PSDB; AAK52534.
                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 226 AA;
                                                                                                                                                      27-APR-2000;
                                            09-AUG-2001
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327 VPDSLLAMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDSIM 386 0; Gaps Query Match 32.0%; Score 800; DB 4; Length 226; Best Local Similarity 99.3%; Pred. No. 5.5e-69; Matches 152; Conservative 0; Mismatches 1; Indels ሯ

74 VPDSLLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNREFFLNVPFDSIM 133 387 ERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQNPKDAEEQVKLKMDLFYRNSADLEQL 446 g 셤 ò

447 YGSAITLNGDQDPYTVPEYIESGIINPLPKKIP 479

ઠે 셤 Search completed: March 18, 2005, 15:17:38 Job time: 173 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2005, 15:09:38 ; Search time 43 Seconds

(without alignments)

1071.810 Million cell updates/sec

1 MADAIAPHRIPPEMPQYGEE......YTVFEXIESGIINPLPKKIP 479

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum Match 0*

Maximum Match 0*

Maximum Match 0*

Maximum Match 100*

Listing first 45 summaries '

Database: PIR 79:*

1: $\overline{D}$ ii: *

2: $\overline{D}$ ii: *

2: $\overline{D}$ ii: *

3: $\overline{D}$ ii: *

4: $\overline{D}$ ii: *

4: $\overline{D}$ ii: *

4: $\overline{D}$ ii: *
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	Description	· · · · · · · · · · · · · · · · · · ·		adenylate kinase (adenylate kinase (a)					adenylate kinases	nucleoside-triphos	adenylate kinase (adenylate kinase P					VIIIABE			adenylate kinase (
SUMMARIES	ΙD	4563	D69334	B95027	B97898	T44404	H97282	C82255	843016	G70307	JS0492	H90019	E84986	AG0378	KIHIMA	ALINOAS APT 127	VIECA	ALBCA Section	690694	C85545	ACI401	A34442	ESPSS4	G83184	AD1815	AC0563	S70734	AE2330	F81154	S61841	1000	286069
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A Otterv	Match		11.0	10.9	10.9	10.9		10.3	10.3		10.0	7.6	7.6	9.6		•	•			•	# c		9.0			•	9.3	9.1	9.1		0	1.
	Score	363.5	274	273	272	272	260	257.5	256.5	255.5	249	242	241.5	240	240	237	235.5	235.5	2000	100	יי כיני		, ,	9 6	232.5	232	231.5	228.5	228.5	228.5	228	;
Result	No.	1	7	m	4	S	ø	7	Φ	6	10	11	12	13	14	15	16	12	· α			3 5	100		3 6	57	25	56	27	28	29	ì

RESULT 2 D69334

		1 KTBCAD	adenylate kinase (nucleoside-triphos adenylate kinase (SS0007 S61843 J01945 S61843 G712247 S77483 B23942 J05893 J05893 J01944 H72100	00000000000000	2115 2205 231 233 233 233 233 233 233 233 233 233	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	225 220.5 220.5 220.5 216.5 216.5 214 214 212 212 212 212 212 212 212 212	,
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ALJGNMENTS	ALIGNMENTS	9.1 214 2 164062. 9.0 215 2 517987 8.8 215 2 551087 8.8 215 2 551843 8.8 227 2 019945 8.6 220 2 672246 8.6 220 2 672246 8.6 241 2 187483 8.6 241 2 185192 8.5 232 2 055893 8.5 220 2 531338 8.5 220 2 501944 8.3 213 2 101944				;			
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gner	gner		ਜ	329 66	389	449	
RESULT 1 S45634 adenylate kinase (BC 2.7.4.3), chloroplast - maize C;6pecies: Zea mays (maize) C;6pecies: Zea mays (maize) C;Accession: S45634; S43039 C;Accession: S45634; S43039 R;6shlitz, B.; Burger, S.; Graffmueller, R.; Deppert, W.R.; Haehnel, W.; Wagner, BLr. J. Biochem. 222, 949-954, 1994 A;Title: Primary structure of maize chloroplast adenylate kinase. A;Rcference number: S45634; MUID:94298837; PMID:8026505	A;Molecule type: protein A;Residues: 1-222 «SGG; A;Cross-references: UNIPROT:P43188 R;Schiltz, E.; Burger, S.; Grafmueller, R.; Deppert, W.R.; Haehnel, W.; Wagner, submitted to the Protein Sequence Database, April 1994 A;Description: Primary structure of maize chloroplast adenylate kinase. A;Reference number: 543039	A; Molecule type: protein A; Residues: 1-22 <scw> C; Genetics: 1-22 <scw> A; Gene: AKI; AdkI A; Map position: 6 A; Genome: nuclear A; Genesianly: adenylate kinase C; Superfamily: adenylate kinase C; Keywords: ATP; chloroplast; phosphotransferase F; 1-222/Product: adenylate kinase #status experimental <mat></mat></scw></scw>	Ouery Match Best Local Similarity 37.3%; Pred. No. 7.9e-18; Matches 78; Conservative 40; Mismatches 90; Indels 1; Gaps 1;	270 RVLLIGPVGSGKSLQAALLAQKYRLVNVCCQQLLKEAVADRTTFGELIQPFFEKEMAVPD 329 : ::	330 SLLMKVLSQRLDQQDCIQKGWYLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389 :::::::	390 TLRRIDPVTGERYHLMYKPPFTMEIQARLLQNPKDABEGQYKLKMDLFYRNSADLEQLYGS 449 : :	450 AIT-LNGDQDPYTVFEYIBSGIINPLPKK 477 : : 187 IIVKVQGDATVDAVFAXIDELGSILEKK 215
T 1 late } cies: s: 10. ession iltz, T. Bic le: Pr	ldues: ldues: lltz, tted t rripti	cule tics: tics: ti AKI posit me: n rfami ords: 2/Pro	y Mat Loca hes	И	m Y	3.	18
RESULT 1 S45634 adenylate N C, Species: C, Date: 10 C, Accession R, Schiltz, Bur. J. Bic. A, Title: Pr A, Reference A, Reference	A;Mole A;Resl A;Cros R;Schi submit A;Desc A;Desc	A;Molecule A;Residues: A;Genetics: A;Gene: Axis A;Map posit A;Map posit C;Superfamil C;Superfamil C;Keywords: F;1-222/Pro	Quer Best Matci	දු දු	충 <u>음</u>	දු පු	රු සි

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Gaps

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; Score 273; DB 2; Length 212;
; Pred. No. 1.2e-11;
46; Mismatches 85; Indels
                 ch 10.9%;
1 Similarity 31.6%;
67; Conservative 4
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                    Query Match
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Matches 67
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              adenylate kinase (EC 2.7.4.3) - Archaeoglobus fulgidus
NyAlternate names: ATP-AMP transphosphorylase
C;Species archaeoglobus fulgidus
C;Date: 05-Dec-1937 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
E;Riclekt, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
E; Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.P.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Anthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A65250; MUID:99049343; PMID:9389475
A;Reterence number: A65250; MUID:99049343; PMID:9389475
A;Retus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-217 <KLE>
A;Feriance add
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Boescription: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
A;Boescription: adenylate kinase
C;Genetics:
A;Boescription: nucleotide-binding motif B #status atypical
F;80-85/Region: nucleotide-binding motif B #status atypical
F;80-85/Region: nucleotide-binding motif B #status atypical
F;80-85/Region: nucleotide-binding motif B #status atypical
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R.Tetcelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A; Althors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Reference number: A95000; MUD:21357209; PMID:11463916
A; Reference number: A95000; MUD:21357209; PMID:11463916
A; Residues: preliminary
A; Residues: 1-212 «KUR»
A; Residues: 1-212 «KUR»
A; Residues: 1-212 «KUR»
A; Residues: L-212 «KUR»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 LLMKVLSORLDOODCIOKGWVLHGVPRDLDOA----HLLARLGYNPNRVFFLAVPFDSIM 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 VVIGIVKERLQQPDC-EKGFILDGFPRTLAQARALDEMLKELNKKIDAVINVVVPEEEVV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 ERLTLERIDPVTGERYHLMYKPP----PTWEIQARLLQNPKDAEEQVKLKMDLFYRNSAD 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Streptococcus pneumoniae
Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenylate kinase [imported] - Streptococcus pneumoniae (strain TIGR4)
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C,Superfamily: adenylate kinase
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adenylate kinase (EC 2.7.4.3) [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-OCt-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B97898
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Er e, R.; LeBlanc, D.J.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc, P.; Sun, P.M.; Winkler, M.S.
J; Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Accession: B97898
A;Accession: B97898
A;Accession: B97898
A;Status: preliminary
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                                                                          331 LLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNR----LGYNPNRVFFLNVPFDSIM
                                                                                                                                                                                271 VLLIGPVGSGKSLOAALLAQKYRLVNVCCGQLLKEAVADRITFGELIQPFFEKEMAVPDS
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14;
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IAHYRAKGLVHDIEGNQDINDVFSDIEKVLTN 210
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RESULT 7
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C;Species Clostridium acetobutylicum
C;Species Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H9728
R;Nolling, J; Braten, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J; Daly, M.J.; Bennett, G; N.; Koonin, E.V.; Smith, D.R.
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A56900; MUID:21359325; PMID:21359325
A;Steatus: preliminary
A;Molecule type: DNA
A;Residues: 1-215 KNIS-
A;Residues: 1-215 KNIS-
A;Residues: 1-215 KNIS-
A;Genetices: UNIPROT:0975J9; GB:AE001437; PIDN:AAK81051.1; PID:gl:S026178; GSPDB:G
C;Genetices: CAC:3112
C;Superfamily: adenylate kinase
                                                                                                                           A; Molecule type: DNA
A; Residues: 1-217 < TAX>
A; Residues: UNIPROT: P38372; EMBL: AB017508; NID: 94512395; PIDN: BAA75292.1; PID: 94
A; Riparami, H; Nakasono. K; Taxaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hira
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Recession: C83669; MUID: 20512582; PMID: 11058132
A; Returus: pre-liminary
A; Residues: 1-217 < STO>
A; Residues: 1-217 < 
Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene-
Reference number: Z22756; MUID:99209008; PMID:10192928
Accession: T44404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 VLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPDS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 LIMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLL-----NRLGYNPNRVFFLNVPP 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 VTIGIVRDRLSQDDC-QNGFLLDGFRTVAQAEALEDILASLDKKLDY----VINIDVPE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 DSIMERLTLRRIDPVTGERYHLMYKPPPTMEI----QARLLQNPKDAEBQVKLKMDLFYR 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 QLLMDRLTGRRVSPTSGRTYHVIFNPPKVBGICDVDGSELIQRDDDKPETVKKRLEVNQK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 RVLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELLQPFFBKEMAVPD 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 10.9%; Score 272; DB 2; Length 217; 1 Similarity 31.3%; Pred. No. 1.4e-11; 66; Conservative 42; Mismatches 83; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.4%; Score 260; DB 2; Length 215; Best Local Similarity 27.6%; Pred. No. 9.5e-11; Matches 60; Conservative 52; Mismatches 79; Indels ;
                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 NSADLEQLY---GSAITLNGDQDPYTVFEYI 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 QAQPLIDFYSEKGYLQNINGBQDISRVFEDI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: adk
C,Superfamily: adenylate kinase
C,Keywords: phosphotransferase
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Best Local Similarity
Matches 66; Conserva
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2 XIILLGPPQAGKGTQAKLISSEFSIFHISTGDIFRANISGKTELGMKAKGYMDKGLLVPD 61

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Cipbedies: Vibrio cholerae
Cipbedies: Ribbidies: Casasion: Casas
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NyAlternate names: ATP-AMP transphosphorylase
Cispecias: Bordetella pertussis
Cispecias: Bordetella pertussis
Cispecias: Bordetella pertussis
Cipate: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
Eightles: A.M.; Sismeinto, O.; Munier, H.; Fabian, H.; Mantsch, H.H.; Surewicz, W.K.; Cra
Eur. J. Biochem. 218, 921-927, 1993
A;Title: Structural and physico-chemical characteristics of Bordetella pertussis adenyla
A;Reference number: S43016; MUID:94109391; PMID:8281944
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A; Experimental source: serogroup O1; strain NI6961; biotype El Tor
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A;Residues: 1-218 <GIL>
A;Cross-references: UNIPROT: P39068; EMBL: Z29715; NID: 9453620; PIDN: CAA82801.1; PID: 94536
A;Experimental source: strain 18323
330 SILMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNR----VFFLNVPFDSI 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenylate kinase VC0986 [imported] - Vibrio cholerae (strain N16961 serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 SLLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVPFLNVPFDSIMERL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 TLRRIDPVTGERYHLMYKPPPTMEIQAR-----LLQNPKDAEEQVKLKMDLFYRNSAD 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DIILGLIKERIAQADC-EKGFLIDGFPRIIPQADGLKEMGINVDYVIEFDVADDVIVERM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 MERLILRRIDPVIGERYHLMYKPPPIMEI----QARLLQNPKDAEEQVKLKMD-----
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10.3%; Score 257.5; DB 2; Length 214;
Best Local Similarity 29.6%; Pred. No. 1.4e-10;
Matches 55; Conservative 47; Mismatches 73; Indels 11,
                                                                                                                                                                                                                                                                                                                                                                                                                ---LFYRNSADLEQLYGSAITLNGDQDPYTVFFYJES 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 PLVVYYRNEAVLK-----SVDGTQDIDKVFEDIRN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: VC0986
A,Map position: 1
C,Superfamily: adenylate kinase
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A, Molecule type: DNA
A, Residues: 1-217 <NAK>
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A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A; Reference number: A70300; MUID: 98196666; PMID: 9537320
A; Reference number: A70300; MUID: 98196666; PMID: 9537320
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-206 < AQRPS
A; Cross-references: UNIPROT: O66490; GB: AE000672; NID: 92982810; PIDN: AAC06438.1; PID: 9298
A; Experimental source: strain VF5
C; Genetics:
A; Gene: kad
C; Function:
A; Mote: magnesium required
C; Function: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
A; Note: magnesium required
C; Superfamily: adenylate kinase
C; Keywords: ATP; P-loop; phosphotansferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ademylate kinase (EC 2.7.4.3) - Aquifex aeolicus
C.Species: Aquifex aeolicus
C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70307
R;Deckert, G.; Marren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
                                                                 form two ADP
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                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLRRIDPVTGERYHLMYKPPPTMEIQ----ARLLQNPKDAEEQVKLKMDLFYRNSADLEQ 445
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gabs
                                                                                                                                                                                                                                                                                                                                            Gaps
C;Genetics:
A;Gene: adk
A;Gene: adk
C;Function: catalyzes reversible phosphorylation of AMP with ATP to i
A;Description: catalyzes reversible phosphorylation of AMP with ATP to i
A;Note: magnasium required
C;Superfamily: ademylate kinase
C;Keywords: ATP; P-loop; phosphorransferase
C;Keywords: ATP; P-loop; phosphorransferase
C;Keywords: nucleocide-binding motif A (P-loop) #status atypical
P;80-85/Region: nucleocide-binding motif B #status atypical
P;30,84,126/Active site: Ser, Asp, His #status predicted
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                                                                                                                                                                                                                                                                                      DB 2; Length 218;
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                                                                                                                                                                                                                                                                                                                                         86; Indels
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                                                                                                                                                                                                                                                                                            10.3%; Score 256.5; DB 2 32.1%; Pred, No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                               34; Mismatches
                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 32.1%
Matches 59; Conservative
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Best Local Similarity
Matches 56; Conserv
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A;ACCESSION: SUBSIST
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A;ACS STEP
A;Cross-references: EMBL:X51329; NID:g40132; PIDN:CAA35713.1; PID:g40135
A;Cross-references: Extain Marburg; cell line PB2
A;Experimental Source: Strain Marburg; cell line PB2
A;Experimental Source: Strain Marburg; cell C. V.; Caldwell, B.; Capano, V.; Carter, N.M.; Cho, S.; Extain, E.
A;Extrain S. D.; Emmerson, P.T.; Entian, C.V.; Caldwell, B.; Pabret, C.; Ferrari, E.
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galier, M.; Marchors: Lauber, J.; Lazarevic, A.; Hilbert, M.; Kurita, K.; Lapidus, A.; Hadino, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Maneel, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Evine, M.; Sadaie, Y.; Sato, T.; Scallon, Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scallon, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scallon, Rieger, M.; Minters, P.; Wipat, A.; Tanaka, T.; Terpetra, P.; Yasumoto, K.; Yata, K.; Yoshida, K.; Ajathors: Yoshikawa, H.F.; Zumateln, R.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A; Title: The complete genome sequence of the Gram-poolstive bacterium Bacillus subtilis.
A; Accession: E65583
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R;Suh, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.
Mol. Microbiol. 4, 305-314, 1990
A,Title: Isolation of a seex homologue from Bacillus subtilis: evidence for a common propagacence number: S08628; MUID:90251170; PMID:2110998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P16304; GB:D00619; NID:g216336; PIDN:BAA00496.1; PID:g216340
R;Yoshikawa, H.; Doi, R.H.
Nucleic Acids Res. 18, 1647, 1990
A;Title: Sequence of the Bacillus subtilis spectinomycin resistance gene region.
A;Reference number: S12680; MUID:90221911; PMID:2139212
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A;Experimental source: strain 168
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adenylate kinase (EC 2.7.4.3) - Bacillus subtilis
NyAlternate names: ATP-AMP transphosphorylase
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: US0492; S12684; S08630; E69583
R;Nakamura, K.; Nakamura, A.; Takamatsu, H.; Yoshikawa, H.; Yamane, K.
J. Biochem. 107, 603-607, 1990
A;Pitle: Cloning and characterization of a Bacillus subtilis gene homologous
A;Reference number: US0490; MUID:90292990; PMID:2113521
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A; Residues: 1-116 < YOS>
A; Cross-references: EMBL: W31102; NID: g1184272; PIDN: AABS9119.1; PID: g143579
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A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. ?
A;Reference number: A84930; MUD:20445173; PMID:10993077
A;Accession: E84986
A;Atcession: E84986
A;Atcession: E94986
A;Atcession: E94986
A;Molecule type: DNA
A;Residues: 1-215 < sgrv
A;Molecule type: DNA
A;Residues: 1-215 < sgrv
A;Residues: 1-215 < sgrv
A;Experimental source: strain APS
A;Experimental source: strain APS
A;Experimental source: strain APS
A;Experimental source: strain APS
C;Genetics:
A;Gene: adk; BU484
C;Superfamily: adenylate kinase
C;Superfamily: adenylate kinase
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Addarylate kinase (EC 2.7.4.3) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date io 2.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0378
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Residues: 1-214 <KUR>
A;Residues: 1-214 <KUR>
A;Residues: 1-214 <KUR>
A;Carasinia pestis WIPPROT:069172; GB:AL590842; PIDN:CAC92354.1; PID:g15981059; GSPDB:G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 ALLVQLIQERLABEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVLIERN 175
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                                                                                                                                                                                                                                                                                                                                                                                                                  270 RVLLLGPVGSGKSLQAALLAOKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 TLRRIDPVTGERYHLMYKPPPTME----IQARLLQNPKDAEEQVKLKMDLFYRNSADLEQ
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                                                                                                                                                                                                                                                                                                                       9.7%; Score 241.5; DB 2; Length; 8.6%; Pred. No. 1.8e-09; ve 44; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                28.6%;
                                                                                                                                                                                                                                                                                                                                                                         52; Conservative
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C,Superfamily: adenylate kinase
C,Keywords: phosphotransferase
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Best Local Similarity 28.6%
Matches 53, Conservative
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Matches
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A; File Mhole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUD:21311952; PMID:11418146
A; Status: preliminary
A; Accession: H90019
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-215 KUR>
A; KESAdues: 1-215 KUR>
A; KESAdues: 1-215 KUR>
A; Comes references: UNIRROT:099540; GB:BA000018; PID:g13702029; PIDN:BAB43321.1; GSPDB:GCGGGENETICER.
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                                                                                                       271 VLILGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPDS 330
                                                                                                                                                                                                       331 LLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQA----HLLNRLGYNPNRVFFLNVPFDSIM 386
                                                                                                                                                                                                                                     63 VTIGIVKERLGKODC-ERGFLLDGFPRIVAQAEALBEILEEYGKPIDYVINIEVDKOVIM 121
                                                                                                                                                                                                                                                                                                    387 BRLTLRRIDPVTGERYHLMYKPPPTWEI----QARLLQNPKDAEEQVKLKMDLFYRNSAD 442
                                                                                                                                        271 VLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPDS 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenylate kinase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90019
                                                                    89; Indels 12; Gaps
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: B49496
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
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                10.0%; Score 249; DB 2; Length 217; 30.4%; Pred. No. 5.5e-10; Live 41; Mismatches 89; Indels 1
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Local Similarity 28.1%; Pred. No. 1.6e-09;
les 56; Conservative 48; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    443 LEQLY --- GSAITLNGDODPYTVF 463
                                                                                                                                                                                                                                                                                                                                                                                                                               443 LEQLY---GSAITLNGDQD 458
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                                   Best Local Similarity 30.4%
Matches 62; Conservative
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C,Superfamily: adenylate kinase
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Best Local S:
Matches 56
                Query Match
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A; Residues: 1-223 <a href="https://doi.org/10.1009/line.com/">doi.org/10.1009/line.com/</a>
A; Molecule type: mRNA
A; Residues: 1-223 <a href="https://doi.org/">doi.org/</a>
A; Cross-references: UNIPROT:P27144; EMBL:X60673; NID:928576; PIDN:CDA43088.1; PID:928577
A; Experimental source: frontal-cortex
A; Note: sequence extracted from NCBI backbone (NCBIN:109644, NCBIP:109645)
C; Gomment: This isozyme is found in the mitochondrial matrix.
C; Genetics:
A; Map position: ortalyzes the reversible phosphorylation of adenine monophosphate with nu A; Note: GTP is preferred to ATP as a substrate
C; Superfamily: adenylate kinase
C; Superfamily: adenylate kinase
C; Superfamily: adenylate kinase
C; Superfamily: adenylate kinase
C; Superfamily: adenylate binage motif A (P-loop) #status atypical
F; 85-89/Region: nucleotide-binding motif B #status atypical
F; 85-89/Region: nucleotide-binding motif B #status predicted
F; 22, 33, 35, 88/Active site: Cys, His, Ser, Asp #status predicted
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Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipacesion: AB1777
Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Joninguez-Bernal, G.; Duchaud, E.; Marapkat, G.; Madueno, E.; Maitournam, A.; Mahathors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mahathors: Kreft, J.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Pitcle: Comparative genomics of Listeria species.
A; A; Accession: AB177
A; Molecule type: DNA
                                                                                                                                      uncleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human NyAlternate names: adenylate kinase 3 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 17-Apr-1993 #sequence revision 23-Mar-1995 #text_change 09-Jul-2004 C;Accession: A42820; S16380; S16381 R;Xu, G.; O'Connell, P.; Stevens, J.; White, R. Genomics 13, 537-542, 1992 A;Atitle: Characterization of human adenylate kinase 3 (AK3) cDNA and mapping of the AK3 A;Reference number: A42820; MulD:92347846; PMID:1639383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 RLTLRRIDPVTGERYHLMYKPPPTWEIQ----ARLLQNPKDAEEQVKLKMDLFYRNSADL 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Mismatches 88; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 IELYKSRGVLHQFSGTETNKIWPYVYTLF----SNKITPIQSK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 EQLYGSAITL---NGDQD-----PYTVFEYIESGIINPLPKK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.6%; Score 240; DB 1;
Best Local Similarity 29.6%; Pred. No. 2.3e-09;
Matches 66; Conservative 45; Mismatches 88
180 SYYHK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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A;Residues: 1-215 <GLA>
A;Cross-references: UNIPROT:0927M8; GB:AL592022; PIDN:CAC97986.1; PID:g16415296; GSPDB:GA
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                       ŝ
                                                                                                                                                                                                                                                                                                                                  330 SLIMKVLSQRLDQQDCIQKGWVLHGVPRDLDQA----HLLNRLGYNPNRVFFLNVPFDSI 385
                                                                                                                                                                                                                                                                                                                                                                                     386 MERLTLRRIDPVTGERYHLMYKPPPT---MEIQ-ARLLQNPKDAEEQVKLKMDLFYRNSA 441
                                                                                                                                                                                                                            270 RVLLLGPVGSCKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPD
                                                                                                                                                                                                                                                   2 KLVLMGLPGAGKGTQAEQIVEKYNIPHISTGDMFRAAMKNNTELGKKAKSFMDNGDLVPD
                                                                                                                                                                                       12; Gaps
                                                                                                                                               Length 215;
                                                                                                                                                                                       87; Indels
                                                                                                                                                 9.5%; Score 237; DB 2;
28.7%; Pred. No. 3.6e-09;
tive 50; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 DLEQLY---GSAITLNGDQDPYTVFEYIE 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: March 18, 2005, 15:21:33
                                                                                                A,Gene: adk
C,Superfamily: adenylate kinase
                                                                                                                                                     Query Match
Best Local Similarity 28.7%
Matches 60; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 18, 2005, 15:08:37; Search time 181 Seconds (without alignments) 1355.171 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-798-773-2 2500 1 MDATIAPHRIPPEMPQYGEE......VIVPEXIESGIINPLPKKIP 479

Scoring table:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Osemae homo sapien Ose figh a rattus norv Osces oryza sativ Osces oryza sativ Osces oryza sativ Ostij7 arabidopsis PallB zea maya (m Osyll arabidopsis Osyll arabidopsis Osyll arabidopsis Osyll arabidopsis Osyll arabidopsis Ostyl arabidocco Ostas fusobacteri Ostyl streptococc Ostas fusobacteri Ostyl burkholderi Ostyl burkholderi Ostyl acinetobact Ostyl a Description SUMMARIES 096MA6
088FB
08N9W9
068FB
060F1B
062C69
062C69
062C60
08V2L1
098V2L1
09FV2T
060T32
060T32
060T32
060T32
060T32
070TM3 KAD FUSNN KAD CLOTE Q7P5X4 KAD ARCFU KAD STRPN KAD STRR6 KAD BACHD Q62HIO KAD STRPY KAD STRA3 * Query Match Length DB 2500 2008 1409 1409 372.5 364.5 363.5 333.5 333.5 313.5 2988 Result

P65204 streptococc Q8k8x1 streptococc Q8k2x4 streptococc Q8p2x4 streptococc Q81j22 bacillus ce Q8xhu4 clostridium Q8ktb7 vibrio chol Q67jw4 symbiobacter O67lw4 symbiobacter O61069 trypanosoma P33068 bordetella Q7wku8 bordetella Q7w7g0 bordetella Q84ffm1 vibrio vuln
KAD STRAS KAD STRR93 KAD STRR93 KAD CLOPE KAD CLOPE OF 7JW4 KAD GLOVI KAD BORPE KAD BORPE KAD BORPE KAD BORPA
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212 212 212 212 212 218 2218 220 218 218 218
10.3 10.3 10.3 10.3 10.3 10.3 10.2 10.2 10.2
2588 2258 2258 2253 2257 255 255 255 255 255
258 258 258 258 257 257 257 256 256 255 255 255 255 255 255 255
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## ALIGNMENTS

RESULT 1

0968M6 PRELIMINARY; PRT; 479 AA. 0968M6; 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Hypothetical protein FLJ32704 (Chromosome 9 open reading frame 98). By B
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EQUENCE FROM N.A. TISSUE=Brain; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 77.0% Matches 368; Conservative
                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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Q68FP8
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
Antachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Astachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Astaplecon M.J., Usdin T.B., Toshiyuki S., Carninci P., Parange C.,
Asta S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Kichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muxry D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Gones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
L. Proc. Natl. Acad. Sci. U.S.A. 99:16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLIKEAVADRITFGELIQPPFEKEWAVPDSLLMKVLSQRLDQQDCIQKGWVLHGVPRDLD 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VILGPPASGKTTIAMMLCKHLNSSLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:005524; F:AFP binding; IEA.
GO; GO:0008603; F:CAMP-dependent protein kinase regulator act...;
GO; GO:0016301; F:Kinase activity; IEA.
GO; GO:0016740; F:Kransferase activity; IEA.
GO; GO:0007165; P:Signal transduction; IEA.
InterPro; IPR000850; Adenylate_kin.
InterPro; IRR003117; RIRa.
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                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 AA; 54925 MW; 9E4EABA3F429B731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2500; DB 2;
100.0%; Pred. No. 3.9e-155;
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ProDom; PD000657; Adenylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AKO57266; BAB71402.1; -. EMBL; BC034776; AAH34776.1; -. EMBL; BC050576; AAH50576.1; -.
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Best Local Similarity 100.1
Matches 479; Conservative
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                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUL-2002)
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                TISSUE=Brain;
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TISSUB-Testis;

TISSUB-Testis;

RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.P., Rubin G.M., Hong L., Bapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., R. Bapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brans S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., R.A. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., R.A. Raha S.S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W., R.A., Milalon D.K., Muzny D.M., Sodergien B.J., Lu X., Gibbs R.A., Sankhing M., Nadan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M. M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., R. Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S., R. Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.B., R. Generation and initial analysis of more than 15,000 full-length human R. R. A. C., Chan R. R. R. Generation and initial analysis of more than 15,000 full-length human
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301 QLLKEAVADRTTFGELLQPFFEKEMAVPDSLLMKVLSQRLDQQDCIQKGWVLHGVPRDLD 360
                                                                            420
                                                                                                                                                                                                                      421 NPKDAEEQVKLKMDLFYRNSADLEQLYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
                                                                                                                                                                                                                                                                1 MDATIAPHRIPPEMPQYGEENHIPELMQNMLEQLLIHQPEDPIPFMIQHLHRDNDNVPRI
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                                                                            QAHLLNRLGYNPNRVPFLANVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ
                                                                                                                  Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the adenylate kinase family.
-!- SIMILARITY: Belongs to the adenylate kinase family.
IN EMBL; BC079446; AAH79446.1; -.
IN EPTO: IPRO00850; Adenylate kin.
PRINTS; PR00094; ADENYLTKNASE.
PRODOM; PD000657; Adenylate kin; 1.
Probom; PD000657; Adenylate kin; 1.
Hypothetical protein; Kinase; Transferase.
SEQUENCE 479 AA; 54965 MW; D2331D51EFC5A15A CRC64;
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Hypothetical protein MCC94995.
Rattur. Rattur.
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                                                                                         SADQPCVDVFYQALITYVQSNHRTNAPFTPRVLLLGPVGSGKSLQAALLAQKYRLVNVCCG 300
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RY TISSUE-Feetis;

RY PubMed-14702039; DOI=10.1038/ng1285;

Ota T., Suzuki Y., Nishikawa T., Otauki T., Sugiyama T., Irle R., Wakamatau A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Waramoto J., Saito K., Wawai Y., Isono Y., Nakamura Y., Maghari K., Ramanoto J., Saito K., Nakamara T., Tanaka T., Ishii S., Murakami K., Wanda K., Tanaka T., Ishia M., Nanda K., Vokoi T., Puruya T., Kikkawa B., Omura Y., Abe K., Kamihara K., Katu Y., Kodaira H., Kondo H., Sugawara M., Rahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa B., Omura Y., Rahashi M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Rahashi-Fujia H., Hara H., Tanase T., Nomura Y., Rahashi-Fujia H., Hara H., Tanase T., Nomura Y., Rahashi-Fujia H., Hara H., Tanase T., Nomura Y., Mashashi-Fujia H., Tanase T., Nomura Y., Rahashi-Fujia H., Hara H., Tanase T., Nomura Y., Mashashi-Fujia H., Tanase T., Nomura Y., Mashashi H., Satoh N., Takami S., Terashima Y., Suzuki O., R. Masazaki M., Watanabe T., Sugiyama A., Takemico M., Kawakami B., Hishigaki H., Watanabe T., Sugiyama A., Takemico M., Kawakami B., Andonyama H., Tahiman A., Takemico M., Kawakami T., Ramazaki M., Watanabe K., Kunagai A., Itakura S., Eulwaya T., Rawabata A., Hikiji T., Kobatake N., Itakura S., Pujiwara T., Rawabata A., Hikiji T., Kobatake N., Itakura S., Pujiwara T., Masunura K., Nakajama Y., Matanabe M., Konatsu T., Mizuun T., Morina M., Rawaban Y., Matanabe M., Komatsu T., Mizuun T., Morina M., Rawaban Y., Matanabe M., Komatsu T., Mizuun T., Masuho Y., Yamashita R., Rawabata A., Hikiji T., Kobatake M., Takhura S., Sabaki M., Watanabe M., Kukuhi H., Masuho Y., Yamashita R., Rawabata M., Hata H., Watanabe M., Kukuhi H., Masuho Y., Yamashita R., Wawamura Y., Ohara O., Isogai T., Sugaya S., Conapite Sequencing and characterization of 21,243 full-India Masai K.
                                                                                                                                                                                                                               QAHLINKLGYNPNRVFFLAVPFDSIMERLTLRRIDPVTGERYHLMYKPPFTMEIQARLLQ 420
                                                                                                                                                                                                                                                                                                     421 NPKDABEQVKLKMDLFYRNSADLEQLYGSAITLNGDQDPYTVFRYIESGIINPLPKKI 478
                                                                                                                                                                                                                                                                                                                                                                           LIQERLA EED CIKQGWILDGIPETREQALRIQTIGITPRHVIVLSA PDTVLIERNLGKRI
                   DPOTGEIXHTTFDWPPESEIONRLMVPEDISELETAOKLLEXHRNIVRVIPSYPKILKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ36127.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Shat N.K.,
Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Butchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Morley R.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,
Richards S., Morley R.C., Shevichenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevichenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 APFTERVLLLIGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 MAVPDSILIMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 MAVPDSLIMKVISQRLDQQDCIQKGWVLHGVPRDLDQAHLIARLGYNPURVFFLNVPFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 IMERLITERIDPVTGERYHLMYKPPPTMEIQARLLQNPKDAEEQVKLKMDLFYRNSADLE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 275; Conservative 0; Mismatches 0; Indels
-I- SIMILARITY: Belongs to the adenylate kinase family. BMBL, AK03946; BAC40168.1; -
BMBL, AK03946; BAC40168.1; -
BMBL, AK03946; BAC40168.1; -
GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0016301; F:KINBER GATCHVILY; IEA.
GO; GO: 0016301; F:KINBER GATCHVILY; IEA.
INTERPRO; IEXO00850; Adenylate_Kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                             275 AA; 31455 MW; B90C76CF137D6C34 CRC64;
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G6P618;
G5-JUL-2004 (TrEMBLrel. 27, Created)
G5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
G5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein MGC76170.
Name=MGC76170;
WantermGC76170;
WantermGC761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
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                                                                                                                                                                                                                                                                            Pfam; PF00406; ADK; 1.
PRINTS; PR00094; ADENYLTKNASE.
PRODOM; PD000657; Adenylate kin; 1.
Kinase; Transferase.
SEQUENCE 275 AA; 31455 MW; B9007
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NCBI_TaxID=8364;
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TISSUE=Embryo;
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NCBI_TaxID=39947;
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Q9FIJ7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
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                                                                                                                                                                                                                                                                                                                                NPKDABEQVKLKMDLFYRNSADLEQLYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
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                                                                   TISSOBERATED (S.)

Klein S., Gerhard D.S.;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-2003) to the ademylate kinase family.

I. SIMILARITY: Belongs to the ademylate kinase family.

EMBL; BC062516; AARE516.1; -..

HSSP; PC05021; TAKE.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006603; F:CAMP-dependent protein kinase regulator act. . .; IEA.

GO; GO:000165; P:Signal transduction; IEA.

InterPro; IPR000850; Ademylate_Kin.

InterPro; IPR003117; KIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAHLLNRLGYNPNRVFFILNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ
  "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                            1 MDATIAPHRIPPEMPOYGEENHIFELMONMLEQLLIHOPEDPIPFMIOHLHRDNDNVPRI
                                                                                                                                                                                                                                                         Gaps
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Eukaryots, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                  Query Match 56.4%; Score 1409; DB 2; Length 485; Best Local Similarity 54.1%; Pred. No. 7.5e-84; Matches 259; Conservative 98; Mismatches 122; Indels
                                                                                                                                                                            PEGNI, PF00406; ADK; 2.

PRINTS; PR00094; ADENYLTKNASE.

ProDom; PD000657; Adenylate_kin; 2.

Hypothetical protein; Kinase; Transferase.

Hypothetical protein; Kinase; Transferase.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative adenylate kinase, chloroplast (ATP-AMP
               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transphosphorylase).
                                                   SEQUENCE FROM N.A.
                                                             IISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 LAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPDSLLMKVLSQRLDQQDCIQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 IKSKYGLVHISAGDLLRABIAAGSENGKRAKEFMEKGQLVPDEIVVNMVKERLLQPDAQE 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 PPPTMEIQARLLQNPKDAEEQVKLKMDLFYRNSADLEQLYGSAIT-LNGDQDPYTVFEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMP transphosphorylase).

AMP transphosphorylase).

Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermarophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 RVIPSYPKILKVISADOPCVDVFYQALTYVQSNHRTNAPFTPRVLLLGPVGSGKSLQAAL
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MEDLINE-99156233; PubMed-10048488;
Agamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima
                                                                               -i- SIMILARITY: Belongs to the adenylate Kinase Lamily.

EMBL; $4004584; EMD09526.1; -.

EMBL; $6000524; F.AKE.

GO; $G0:000524; F.ATP binding; IEA.

GO; $G0:0005301; F.Kinase activity; IEA.

GO; $G0:0016776; F.Engephotransferase activity; phosphate grou.

GO; $G0:0016776; F.Engephotransferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 14.9%; Score 372.5; DB 2; Length 290; Local Similarity 34.3%; Pred. No. 2e-16; Indels 25, 1eg 86; Conservative 41; Mismatches 99; Indels 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-0cr-2003 (Rel. 42, Created)
10-0cr-2003 (Rel. 42, Last sequence update)
25-0cr-2004 (Rel. 45, Last annotation update)
Probable adenylate kinase 2, chloroplast precursor (EC
Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the adenylate kinase family.
EMBL; AP004584; BAD09526.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 AA; 31816 MW; 058918D67A71E8D2 CRC64;
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PRODOM; PD000657; Adenylate_Kin; 1.
TIGREAM; TIGREAM; TIGREAM; TERPOSITE; PROSITE; PROSITE; F800113; ADENVLATE_KINASE; 1.
Kinase; Transferase.
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InterPro; IPR006259; Adenyl_kin_sub
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273 DKQLTSSLDKK 283
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SEQUENCE FROM N.A.

STRAINE-V. Columbia;

WEDLINE-22954850; PubMed-14593172; DOI=10.1126/science.1088305;

Yamada K., Lim J., Dabe J.M., Chen H., Shinn P., Palm C.J.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Tang C.C., Dong C.H., Lee J.M., Toriumi M.J.,

Chan M.M., Tang C.C., Dondera C.S., Beng J.M., Akiyama K., Ansari Y.,

A Rawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Rawa T., Banh J., Banno F., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Rababitzaki Y., Johnson-Hopson C., Hanan V.W., Ilda K., Karnes M.,

Khan S., Koesema E., Ishida U., Jiang P.X., Jones T., Kawai J.,

Satou M., Tamse R., Vaysberg M., Wallender B.K., Wong C., Yamamura Y.,

Satou M., Tamse R., Vaysberg R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Emptopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 RVLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPD 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 KIMISGAPASGKGTQCELITHKYGLVHISAGDLLKARIASGSENGRRAKEHMEKGQLVPD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 SLIMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 TLRRIDPVTGERYHLMYKPPPTWEIQARLLQNPKDAEEQVKLKMDLPYRNSADLEQLYGS 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 283;
                                                                                                                                                                                                                                                   genome.";
Science 302:842-846(2003).
-!- FUNCTION: This small ubiquitous enzyme is essential for maintenance and cell growth (By similarity).
-!- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
-!- SUBCELLUIAR LOCATION: Chloroplast (By similarity).
-!- SIMILARITY: Belongs to the adenylate family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%; Score 364.5; DB 1; Length; 36.4%; Pred. No. 6.4e-16; ative 39; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 79 ATP (By similarity).
283 AA; 31452 MW; 1461D1A36P2DF4E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 -AITLNGDQDPYTVFEYIESGIINPLPKK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 ITIKIEGNRSKEEVFAQIDSSLSELLQER 274
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ID KADC_MAIZE
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SEQUENCE
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222 AA.

PRT;

STANDARD;

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NOTE-REF. IN WW-24867; METHOD-Ellectrospray; RANGE-1-222;
NOTE-REF. I.
                                                                                                                              Zea mays (Maize).
Bukaryock; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                             MEDLINE-94298837; PubMed-8026505;
Schiltz E., Burger S., Grafmueller R., Deppert W.R., Haehnel
Wagner E.;
                                                                                                                                                                                                                                                                                                                                      "Primary structure of maize chloroplast adenylate kinase.";
Eur. J. Biochem. 222:949-954(1994).
P43188;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Adenylace kinase, chloroplast (EC 2.7.4.3) (ATP-AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (By similarity)
                                                                                                                                                                                                                                           SEQUENCE, AND MASS SPECTROMETRY.
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41 HDLLERPIPPQIVIAGPPGSGKGTQCQAIVERFGVVHISSGDLLRAEVAAGTEVGKMAET 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 342; DB 2; Length 26 ilarity 31.3%; Pred. No. 1.8e-14; Conservative 54; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 AA; 30060 MW; BAB658834D6984E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Friedlin;
MEDLINE=99146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L.,
Smith D.F.;
                                                                                                                                                                                                         438 RNSADLEQLYGSAI-TLNGDQDPYTVFE 464
                                                                                                                                                                                                                                569
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PROSITE; PS00113; ADENYLATE KINASE; 1.
Kinase; Transferase.
SEQUENCE 269 AA; 30060 MW; BARGSAR?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006559; Adenylate kin.
InterPro; IPR006259; Adenyl kin sub
                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                  PRT;
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PRINTS; PR00094; ADENYLTKNASE.
                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible adenylate kinase
                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 81; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=L6294.05;
Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 NHRTNAPFTPRVILLGPVGSGKSLQAALLAQKYRLVNVCGQLLKEAVADRTTFGELIOP 319
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                                                                                                                                                                                                                                                                                                 330 SLLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389
                                                                                                                                                                                                                                                                                                                        390 TLRRIDPVTGERYHLMYKPPPTMEIQARLLQNPKDAEEQVKLKMDLFYRNSADLEQLYGS 449
                                                                                                                                                                                                                                                                                                                                                                                                      99
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                                                                                                                                                                                                                      270 RVILLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPD
                                                                                                                                                                                                                                                 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                    Gaps
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GO, GO:0006524; F:ATP binding; IEA.

GO, GO:0016301; F:Kinase activity; IEA.

GO; GO:0016740; F:Transferase activity, phosphate grou.

GO; GO:0016740; F:Transferase activity; IEA.

InterPro; IPR00850; Adenylate Kin.

InterPro; IPR00855; Adenyl kin. sub.

InterPro; IPR007862; ADK.lid.

Pfam; PF05191; ADK.lid.

PRINTS; PR00094; ADENYLTKNASE.

PRINTS; PR00094; Adenylate_Kin; 1.
                                                                                                                                                                                    1;
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                                                                                                                                        ; Score 363.5; DB 1; Length 222; ; Pred. No. 5.5e-16; 40; Mismatches 90; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAINS-CL Brener.
STRAINS-CL Brener.
SURAINS-CL Brener.
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: ABOLOGS to the adenylate kinase family.
EMBL; POSOSZ: AAOUSOUS.1; -1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 AA; 29337 MW; BBCE886E43115F8C CRC64;
                                                                                                      24867 MW; 19257324F8B7630D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Similarity .30.6%; Pred. No. 6.7e-16;
32; Conservative 53; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TICREAMS, TIGRO1351, adk; 1.
PROSITE, PSO0113, ADENYLATE_KINASE; 1.
Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                   Match 14.5%;
Local Similarity 37.3%;
es 78; Conservative 4
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                                   183
188
197
220
222 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLASEDCIKOGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVLIERNLGKRIDPQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
                                                           FFEKEMAVPDSLLMKVLSQRLDQQDCTQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLN 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 YGEENHIFELMQNMLEOLLIHQPEDPIPFMIQHLHRDNDNVPRIVILGPPASGKTTIAMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Gaps
                                             380 VPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQ--ARLLQNPKDAEEQVKLKMDLFY
              Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                    Chan H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 269;
                                                                                                                                                                                                                                                                                                                                                             "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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195 ILIDRCVGRRLDPVTGKIYHIKNYPPESDEIKARLVTRPDDTEEKVKARLQIYKQNSEAI 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 RRIDPVTGERYHLMYKPPPTMEIQARLLQNPKDABEQVKLKMDLFYRNSADLEQLYGSAI 451
                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:000524; F:ATP binding; IEA.
GO; GO:000524; F:Kinase activity; IEA.
GO; GO:0016710; F:phosphotransferase activity, phosphate grou. . .; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IFR000850; Adenylate kin.
InterPro; IFR006259; Adenylate kin.
Fam; PF00466; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 LLIGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFBKEMAVPDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 25, Last sequence update)
Adenylate kinase-like.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE FROM N.A.
Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.8%; Score 320; DB 2; Length 217; llarity 34.4%; Pred. No. 3.7e-13; Conservative 42; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: Belongs to the adenylate kinase family. EMBL, APO00421; BAB10023.1; -- HSSP; P43188; 1ZAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AA; 24065 MW; 76FBED1964ACD04E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
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                                                                                                                                        217 AA.
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PRINTS, PRODOGS, ADENTITIVANSE.
PRODOM, PDODOGS7, Adenylate_kin; 1.
TIGRFAMS; TIGRO1351, adk, 1.
PROSITE, PSO0113; ADENYLATE_KINASE; 1.
                                                    255 ISAYSDVMVKIDANRPKEVVFE 276
                              444 EQLYGSA-ITLNGDODPYTVFE 464
                                                                                                                                        PRT;
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27,
27,
                                                                                                                                        PRELIMINARY;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adenylate kinase 4.
Name=AdK4;
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62; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                        O9FYO7
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Matches
                                                                                                         RESULT 11
Q9FYQ7
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GEIYHTTFDWPPESE--IQNRLMVPEDISELETAQKLLEYHRNIVRVIPSYPKILKVISA 242
                    264 NAPPTPRVLLIGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 NEPL--KVMISGAPASGKGTQCELIVHKFGLVHISTGDLLRAEVSSGTDIGKRAKEFMNS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 EMAVPDSLLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFD 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 GSLVPDEIVIAMVAGRLSREDAKEHGWLLDGFPRSFAQAQSLDKLNVKPDIFILLDVPDE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 SIMERLTLRRIDPVTGERYHLMYKPPPTWEIQARLLQNPKDAEEQVKLKMDLFYRNSADL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005524; F:ATP binding; IEA.
GO:0015301; F:kinase activity; IEA.
GO:0016776; F:phosphotransferase activity, phosphate grou. . .; IEA.
GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Yanada K., Liu S.X., Chusch H.L., Toriumi M., Yu G., Boweer L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryocks; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacees; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 13.3%; Score 333.5; DB 2; Length 588; 1 Similarity 33.7%; Pred. No. 1.7e-13; 68; Conservative 47; Mismatches 84; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                588 AA; 65738 MW; 3AA0B81ABFC4B62B CRC64;
                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative adenylate Kinase.
                                                                                                                                                                    588 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PP00406; ADK; 1.

PRINTS; PR00094; ADENYLTKNASE.

ProDom; PD000657; Adenylate kin; 1.

TIGRFAMS; TIGR01351; adk; 1.

PROSITE; PS00113; ADENYLATE KINASE; 1.

Kinase; Transferase.
                                                                                                                                                                    PRT;
                                                                                      NRPEAAITKDITEYLO-NH 266
                                                             243 DOPCVDVFYQALTYVQSNH 261
                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                                               Name=At5g35170
                              189
                                                                                        249
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KAD OCEIH
QBETW3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 LCKHLNSSLLTLENLILNEFSYTATEARRL---YLQRKTVPSALLVQLIQERLAEEDCIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 QGWILDGIPETREOALRIQTLGITPRHVIVLSAPDTVLIERNLGKRIDPQTGEIYHTTFD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPPESEIQNRIMVPED-ISELETAQKILEYHRNIVRVIPSYPKILKVISADQPCVDVFYQ 252
                                                                                                                                                                                                                                                                                                                                                                                                           17 YGEENHIFELMQNMLEQLLIHQPEDPIPPMIQHLHRDNDNVPRIVILGPPASGKTTIAMW 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                  13 YPEEKHINTLLEELFHDVMVHLPDDPLQPLHAL--DRKTTLRLMVLGPSGAGKRTQSRR
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                  DB 2; Length 260;
                   Bountier L.A., Miranda M.R., Canepa G.E., Pereira C.A.;
Bountier G. Miranda M.R., Canepa G.E., Pereira C.A.;
Bounitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
C. -1- SIMILARITY: Belongs to the adenylate kinase family.
R. EMBL; AYS-6734; AAS-20418.1; -.
R. HSSP; P05082; JAKE.
R. GO; GO:0005524; F:ATP binding; IEA.
R. GO; GO:0016301; F:kinase activity; IEA.
R. GO; GO:0016740; F:transferase activity; IEA.
R. Pfam; PF00406; ADK; 1.
R. Probom; PD000657; Adenylate_kin. 1.
R. Probom; PD000657; Adenylate_kin; 1.
R. Rinase; Transferase.
J. SEQUENCE 260 AA; 23610 MW; OCCA67290386081F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z8-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 45, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (AIP-AMP transphosphorylase).
Name=adk; OrderedLocusNames=TTE2271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoannerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- CATALYTIC ACTIVITY: APP + AMP = 2 ADP.
-1- SUBUNIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the adenylate kinase family.
                                                                                                                                                                                                                                                                                                                               12.5%; Score 313.5; DB 2; Length 30.2%; Pred. No. 1.2e-12; ive 52; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.4.
Loca 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EI 249
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Q8R7X4;
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KAD_THETN
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use by non-profit institutions as long as its content is in. no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 BVTNRIVEDRLEKEDC-KKGFLLDGYPRNIPQABELDKFLEBRGHSLTAVINIQVEREAL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 SLIMKVISORIDOODCIOKGWVLHGVPRDLDOAHLINRL----GYNPNRVFFLNVPFDSI 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=HTEB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
Takani H., Takaki Y., Uchiyama I.;
Takani I., Tak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
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-!- FUNCTION: This small ubiquitous enzyme is essential for enritherance and cell growth.

maintenance and cell growth.

-!- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.

-!- STBUTTL ACTIVITY: ATP + AMP = 2 ADP.

-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).

-!- SUBCELLUIAR LOCATION: Cytoplasmic kinase family.

-!- SIMILARITY: Belongs to the adenylate kinase family.
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10-607-2003 (Rel. 42, Last sequence update)
25-607-2004 (Rel. 45, Last annocation update)
26-007-2004 (Rel. 45, Last annocation update)
Name-adk; OrderediocusNames-OB0140;
Oceanobacillus iheyensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probom; PD00065/; ... adk; 1.
TIGRFAMS; TIGRO1351; adk; 1.
PROSITE; PS00113; ADENYLATE KINASE; 1.
PROSITE; PS00113; ADENYLATE KINASE; 1.
ATP Complete proteome; Kinase; Transferase.
ATP (By similarity).
ATP (By similarity).
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28.6%; Pred. No. 2.6e-11;
iive 61; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 DLEQLY---GSAITLNGDQDPYTVFEYIESGII 471
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             HSSP; P27142; IZIN.
HAMAP; MF 00235; -; 1.
Interbro; IPR000629; Adenyl kin sub.
Interbro; IPR000850; Adenylate kin.
Interpro; IPR000861; ADK_lid.
Pfam; PF00406; ADK; 1.
PRINTS; PR00094; ADENYIRNASE.
Probom; PD0000657; Adenylate_kin; 1.
                                                                                                                                                                                                                                                                                            EMBL; AE013171; AAM25415.1; -.
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EMBL, APO0453; BAC12096.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 VLLIGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRITFGELIQPFFEKEMAVPDS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 LLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQA----HLLNRLGYNPNRVFFLNVPFDSIM 386
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WEDILINELSTRAY 199.

WEDILINELSTRAY 199.

WEDILINELSTRAY 199.

WEDILINELSTRAY 199.

B. 18-Sayed N.M.A., Ghedin E., Song J., MacIeod A., Eningaud F.,

B. 18-Sayed N.M.A., Ghedin E., Song J., MacIeod A., Eningaud F.,

B. 18-Barian V., Wahalak H.G., Lin X., Mason T., Hannick L., Caler E.,

B. 18-Barian G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,

Nan Aken S., Utterback T., Haas B., Koo H.L., Umayam L., Suh B.,

Nan Aken S., Utterback T., Haas B., Koo H.L., Umayam L., Suh B.,

Adams M.D., Fraser C.M., Donelson J.B.;

Adams M.D., Fraser C.M., Donelson J.B.;

M.Cleic Acids Res 31:4856-4863(2003).

I. SIMILANITY: Belongs to the adenylate kinase family.

RHSP, POGOSI 184.

RHSP, POGOSI 184.

ROJ, GO:000554; F.ATP binding; IEA.

ROJ, GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82; Indels 12; Gaps
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ORKNames-Tb927.2.5660;

Trypanosoma brucei.

Bukaryotam ablenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                 HAMAP, MESE', KZIAZZ, 12.1.
HAMAP, MF 00235; -; 1.
HAMAP, MF 00255; -; 1.

InterPro; IPR000850; Adenylate kin.
InterPro; IPR001862; Abx_lid.
InterPro; IPR001863; Abx_lid.
INTER; PR00194; ADENYLIXNASE.
INTERPROSITE; PR00113; ADENYLATE KINASE; 1.
INTERPROSITE; PS00113; ADENYLATE KINASE; 1.
INTERPROSITE PS00113; ADENYLATE KINASE; 1.
INTERPROSITE; PS00113; ADENYLATE KINASE; 1.
INTERPROSITE; PS00113; ADENYLATE KINASE; 1.
INTERPROSI
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Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last anno
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233 YPKILKVISADQPCVDVFYQALTYVQSNHRTNAPFTPRVLLLGPVGSGKSLQAALLAQKY 292
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11.4%; Score 286; DB 2; Length 260;
Best Local Similarity 27.2%; Pred. No. 7.8e-11;
Matches 67; Conservative 51; Mismatches 116; Indels 12; Gaps
InterPro; IPR000850; Adenylate_kin.
Pergen; PP00406; ADK; 1.
Probom; PD000657; Adenylate_kin; 1.
Kinase; Transferase.
SEQUENCE 260 AA; 29339 MW; 8F15B485E68B1FC7 CRC64;
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Issued_Patents_AA:*

1. /cgn2_6/ptodata1/liaa/5A_COMB.pep:*
2. /cgn2_6/ptodata1/liaa/6A_COMB.pep:*
3. /cgn2_6/ptodata1/liaa/6A_COMB.pep:*
4. /cgn2_6/ptodata1/liaa/6B_COMB.pep:*
5. /cgn2_6/ptodata1/liaa/PcTUS_COMB.pep:*
6. /cgn2_6/ptodata1/liaa/PacTUS_COMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Seminary Condition		, ,						5.70	Sequence 5. Appli	6				Semience 3, Appli	; ;	. ~	, -	-	314	•	· 4			Seguence 10363, A	Sequence 10366, A		
SUMMARIES	ID.	US-10-141-634-2	US-10-141-634-4	US-09-328-352-5675	US-09-583-110-4124	US-09-107-433-4765	US-09-513-999C-7572	US-09-134-001C-3289	US-09-710-279-1580	US-08-829-027-5	US-09-225-366-5	US-09-949-016-9245	US-09-489-039A-12712	US-09-543-681A-7057	US-08-829-027-3	US-09-225-366-3	US-09-252-991A-21097	US-09-149-476-377	US-08-829-027-1	US-09-225-366-1	US-09-540-236-3142	US-08-829-027-4	US-09-225-366-4	US-09-134-000C-5802	US-09-949-016-10565	US-09-949-016-10566	US-09-438-185A-246	US-09-107-532A-3675	
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Sequence 18000. A	ď	Semionor 12000	7	1:	3;	٠,	Sequence 1/698, A		, ,			200	Sequence 2, Appli	Sequence 2. Appli	٠,	, ,	٠,	sednence 15, Appl	Sequence 15, Appl
US-09-248-796A-18000	US-08-879-561-5	US-09-902-540-13555	IIS-08-879-561-11	TS-09-949-016-11709	11S+08-87-018-11	US-09-04-7962-17698	US-09-270-767-44420	US-09-198-4522-1179	118-09-513-9990-5448	11S-09-248-7968-16969	TIS-00-252-0018-20204	TIO 00 C41 0148 D	2-W-23-03-W-2	US-08-648-650A-2	US-09-183-266A-2	US-09-902-540-11337	TIS-09-248-520-15	CT-07C-017-C0-C0	US-09-549-108-15
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161	153	149.5	149	149	143	141.5	141	139.5	124.5	120.5	120	119.5		C. KTT	119.5	115	113.5		113.5
28	53	30	31	32	33	34	35	36	37	38	39	40		<b>.</b>	42	43	44		n T

## ALIGNMENTS

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## Sequence 4124, Application US/09583110

## SERNERAL INFORMATION:

## TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

## TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

## TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

## TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

## TITLE OF INVENTION: Number: US 09/107,433

## PRIOR PILING DATE: 1998-06-30

## PRIOR PILING DATE: 1998-06-30

## PRIOR PILING DATE: 1998-05-12

## PRIOR FILING DATE: 1997-07-02

## NUMBER OF SEQ ID NOS: 5322

## NUMBER OF SEQ ID NOS: 5322

## LEAVERY: 21-3

## LEAVERY: 21-3
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                                                                                                                           387 ERLTLRRIDPVTGERYHLMYKPPPTM----ELQARLLQNPKDAEEQVKLKMDLFYRNSAD 442
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64 VSDELIIGLVKERIAQPDCV-NGCIFDGFPRTIPQARALEKEGISIDHVIEIDVFDEEIV 122
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Sequence 4765, Application US/09107433
Patent No. 68007414
GENERAL INFORMATION
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A DOUCETTC ACID AND AMINO ACID
TITLE OF INVENTION: SUCHENCE RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 VLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPDS
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                                                                                                                                                                                                                                                                                                                                                                 180 TEQLVGFYQGRAASGENAPTYDKLDGLRTIEDVQKDLFNILDK 222
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ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.6%; Pred. No. 5.5e-20;
Matches 67; Conservative 46; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 Y-----GSAITLNGDQDPYTVFEYIESGIIN 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 IAHYRAKGLVHDIEGNÖDINDVFSDIEKVLTN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-583-110-4124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-107-433-4765
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; Sequence 4, Application US/10141634
; Patent No. 6734010
; Patent No. 6734010
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6734010e1 Human Kinases and Polynucleotides Encoding the Same
; TITLE OF INVENTION: No. 6734010e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5675, Application US/09328352

Becent No. 6562958

GENERAL INFORMATION:
APPLICAMT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5675
LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 MERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLLQNPKDAEEQVKLKMDLFYRNSADLEQ 445
                                                                           QAHLLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
                                                                                                                                4 FFWRIILLGPPGAGKGTQAQLICKRYNIPQISTGDMLRAAIREGTELGLKAKSVWESGGL
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11.2%; Score 280.5; DB 4;
Best Local Similarity 29.6%; Fred. No. 9.8e-21;
Matches 66; Conservative 47; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
19.6%; Score 491; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.2e-43;
Matches 94; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 LYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP
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US-09-328-352-5675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-141-634-4
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Sequence 3289, Application US/09134001C

Retent No. 6380370

GENERAL INFORMATION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS FILE REFERENCE: GTC-0.7

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER: US 60/055,779

SEQ ID NO 3289

LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 LIMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNR----VFFLNVPFDSIM 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75; Indels 19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
10.0%; Score 249; DB 4; Length 66;
Best Local Similarity 74.2%; Pred. No. 2.7e-18;
Matches 49; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
9.9%; Score 247.5; DB 3
Best Local Similarity 28.9%; Pred. No. 2.6e-17;
Matches 57; Conservative 46; Mismatches 75
                                                                                                                                           CANTON: 41

OTHER INFORMATION: Xaa=1le or Asn
FEATURE:
NAME/KEY: UNSURE
LOCATION: 46
OTHER INFORMATION: Xaa=Leu or Val
FEATURE:
LOCATION: 51
CANTON: 51
OTHER INFORMATION: Xaa=Pro or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3289
                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 52
; OTHER INFORMATION: Xaa=Asp or Glu
US-09-513-999C-7572
                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||
61 HLHRDS 66
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SOFTWARE: Patent.pm
SEQ ID NO 7572
                                                                                                                              NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: UNSURE
LOCATION: 52
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 LLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNR----LGYNPNRVFFLNVPFDSIM 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 BRLTLERIDPVTGERYHLMYKPPPTMELQARLLQNPKDAEEQVKLKMDLFYRNSADLEQL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.9%; Score 273; DB 4; Length 216;
Best Local Similarity 31.6%; Pred. No. 5.6e-20;
Matches 67; Conservative 46; Mismatches 85; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7522, Application US/09513999C
Retent No. 6783961
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Dunclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PARENT FILING DATE: 19.02.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT PILING DATE: 1999-0.2-24
PRIOR PPLICATION UNMERR: US 60/122,487
PRIOR PILING DATE: 1999-0.2-26
NUMBER OF SEQ ID NOS: 36691
                                                                                                                                                                                          APPLICATION DATA:

FILING DATE: May 12, 1999

APPLICATION NUMBER: 60/051531

FILING DATE: May 12, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40, 489

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-8277

INFORMATION FOR SEQ ID NO: 4765:

SEQUENCE CHARACTERISTICS:

LENGTH: 216 amino acids

TYPE: amino acid

TOPOLOGY: linear

NOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 IAHYRAKGLVHDIEGNÖDINDVPSDİEKVLTN 214
                                                                                         SOFTWARE: «Unknown»
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...216
SEQUENCE DESCRIPTION: SEQ ID NO: 4765:
                      MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <UNKNOWN>
OPERATING SYSTEM: <UNKNOWN>
       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-513-999C-7572
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,027
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Patent No. 6001624
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                                                                                                                                                                                                                                                                                                                                                                                                                                   29.68;
                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 29.6
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM MEDIUM TYPE: Diskett
            PRIOR APPLICATION: 435
APPLICATION NUMBER:
FILTNG NAME
                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                  GenBank
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FILING DATE: He CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                ; LIBRARY: Geni
; CLONE: 28577
US-08-829-027-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-225-366-5
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                              TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 LLMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNR----VFFLNVPFDSIM 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCRAMATION:
GENERAL INCRAMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILLS REFERENCE: P191880US
CURRENT APPLICATION NUMBER: US/09/110,279
CURRENT FILING DATE: 2000-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1580
LENGTH: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence
US-09-710-279-1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08829027
Patent No. 5885160
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSER: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.7%; Score 242.5; DB 4; Length 2
Best Local Similarity 28.4%; Pred. No. 8.3e-17;
Matches 56; Conservative 47; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,027
                                                                                                                  RESULT 8
US-09-710-279-1580
; Sequence 1580, Application US/09710279
; Patent No. 6703492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 ILEYYNNKGVLKNIDGS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---FYRNSADLEQLYGS 449
                                                   189 ILEYYNNKGVLKNIDGS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                               ---FYRNSADLEQLYGS 449
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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388 RLTLRRIDPVTGERYHLMYKPPPTMEIQ----ARLLQNPKDAEEQVKLKMDLFYRNSADL 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 IELYKSRGVLHQFSGTETNKIWPYVYTLF----SNKITPIQSK 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.6%; Score 240; DB 2;
19.6%; Pred. No. 1.6e-16;
.ve 45; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PSESEEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc.
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMONICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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Patent No. 660570, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION
TITLE OF INVERNION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVERTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVERTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT PELIGOR DATE: 2000-04-05
CURRENT PILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7057
LENGTH: 223
LEN
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Sequence 12712, Application US/09489039A

Batent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TOTREMY FAPILICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
TEMPORE SEG ID NOS: 14342
                          330 SLLMKVLSQRLDQQDCIQKG--WVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDSIMB 387
                                                                        117 HVITRLMMSELEN----RRGQHWLLDGFPRTLGQAEALDKI-CEVDLVISLNIPFETLKD 171
                                                                                                                                                        388 RLTLRRIDPVTGERYHLMYKPPPTWEIQ----ARLLQNPKDAERQVKLKMDLFYRNSADL 443
                                                                                                                                                                                                          57 VPRIVILGPPASGKTTIAMWLCKHLNSSLLTLENLI---LNEFSYTATEARRLYLQRKTV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 PSALLVQLIQERIAEEDCIKQGWILDGIPETREQALRIQTIGITPRHVIVLSAPDTVLIE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 RNLGKRIDPQTGEIYHTTFDWPPESEIQN-----RLMVPEDISELETAQKLLEYHRNIVR 228
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                                                                                                                                                                                                                                                                                              444 EQLYGSAITL---NGDQD-----PYTVFEYIESGIINPLPKK 477
                                                                                                                                                                                                                                                                                                                                           232 IBLYKSRGVLHQFSGTETNKIWPYVYTLF---SNKITPIQSK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRGANISM: Klebsiella pneumoniae US-09-489-039A-12712
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; ORGANISM: Proteus mirabilis
US-09-543-681A-7057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 VIPSYPK 235
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US-09-543-681A-7057
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| Retent No. 6812339
| GENERAL INPORMATION:
| APPLICAMY: VENTER, O. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| CURRENT APPLICATION NUMBER: US/09/949, 016 |
| PRIOR APPLICATION NUMBER: 60/211, 755 |
| PRIOR APPLICATION NUMBER: 60/231, 768 |
| PRIOR PLING DATE: 2000-10-03 |
| PRIOR PLING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE FRAISE FRAISE FRAISE FRAISE FRAISE FRAISE FRAISE FRAISE PROFILES |
| SOFTWARE FRAISE FRAISE PRESENCE FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 RITLRRIDPVTGERYHLMYKPPPTMEIQ----ARLLONPKDAEEQVKLKMDLFYRNSADL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 RVLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMAVPD 329
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9.6%; Score 240; DB 3; Length 223;
Best Local Similarity 29.6%; Pred. No. 1.6e-16;
Matches 66; Conservative 45; Mismatches 88; Indels 24; Gaps
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                              NAME: Billings, Lucy J.
REGISTRATION UNUBER: 36,749
REPRENCE/DOCKET NUMBER: PF-02
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 223 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear IMMELATE SOURCE: LIBRARY: Genbank CLONE: 28577
ATTORNEY/AGENT INFORMATION:
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; SEQ ID NO 9245
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9245
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US-09-225-366-5
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330 SLIMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLLNVPFDSIMERL 389
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270 RVLLIGPVGSGKSLOAALLAOKYRLVNVCCGQLLKGAVADRTTFGELIQPFFEKEMAVPD 329
                   390 TLRRIDPVTGERYHLMYKPPPTMEIQ----ARLLONPKDAEEQVKLKMDL------
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                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09225366

Sequence 3, Application US/09225366

Patent No. 6001624

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Purvi

TITLE OF INVENTION:

APPLICANT: Shah, Purvi

TITLE OF INVENTION:

CORRESPONDENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Forter Drive

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 227;
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; Pred. No. 7.8e-16;
37; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FEATURE OF Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0256 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY AGENT INFORMATION:
ATMAE: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-OTELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.3%;
Best Local Similarity 30.4%;
Matches 59; Conservative 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 227 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                       :|| || |:
186 YYRKKGVLETFSGT 199
                                                                                                                                                                                                                436 FYRNSADLEQLYGS 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
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                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-225-366-3
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                                                                                                                                                                                                                                                           267 FTPRVLLLGPVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEMA 326
                                                                                                                                                                    327 VPDSLIAMKVLSQRLDQQDCIQKGWVLHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDSIM 386
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 17;
                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 227;
                              ; Score 236.5; DB 4; Length 223; ; Pred. No. 3.7e-16; 41; Mismatches 82; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Purvi

APPLICANT: Shah, Purvi

TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.3%; Score 233.5; DB 2; Best Local Similarity 30.4%; Pred. No. 7.8e-16; Matches 59; Conservative 37; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,027
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION DATE:
ATTORNEY DATE:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08829027
Patent No. 5856160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                       Query Match
Best Local Similarity 28.7%
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIPICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 184 TAPLVSYY 191
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217576
                                                                                                                                                                                                                                                                                                                  440 SADLEQLY 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-829-027-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-829-027-3
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Sequence 3020, Apsequence 2, Appli
Sequence 25, Appli
Sequence 25, Appl
Sequence 22, Appl
Sequence 868, App
Sequence 1179, Appli
Sequence 4, Appli
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Sequence 4, Appli
Sequence 268668,
                                                                                                                                                         March 18, 2005, 15:20:58; Search time 149 Seconds (without alignments) 1062.612 Million cell updates/sec
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Sequence 3020,
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1: (cgn2 6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

3: (cgn2 6/ptodata/2/pubpaa/NGO7_PUBCOMB.pep:*

3: (cgn2 6/ptodata/2/pubpaa/USO6_NEW_PUB:*

5: (cgn2 6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

6: (cgn2 6/ptodata/2/pubpaa/USO7_NEW_PUB:*

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9: (cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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15: (cgn2 6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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5 US-10-094-749-3020

103-10-104-047-322-2

5 US-10-311-034-25

4 US-10-164-868-87

US-09-764-868-87

US-09-764-868-88

US-09-764-868-1179

US-10-141-634-4

T US-10-141-634-4

7 US-10-141-634-592-68668

6 US-10-437-963-120944
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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RESULT.

1 US-10-141-634-2

1 Sequence 2, Application US/10141634

2 Publication No. US20030008365A1

3 FULICATI X16, Qiongshu

3 APPLICANT: Yu, Xuanchuan

4 APPLICANT: Yu, Xuanchuan

3 APPLICANT: Walke, D. Wade

4 APPLICANT: Walke, D. Wade

5 TILE REFERENCE: LEX-034-USA

6 CURRENT FILING DATE: 2003-05-08

7 FILE REFERENCE: LEX-034-USA

6 CURRENT FILING DATE: 2001-05-09

7 FILE REPERENCE: LEX-034-USA

7 CURRENT FILING DATE: 2001-05-09

7 FILE REPERENCE: LEX-034-USA

7 CURRENT FILING DATE: 2001-05-09

7 FILE REPERENCE: LEX-034-USA

7 CURRENT FILING DATE: 2001-05-09

7 FILE REPERENCE: LEX-034-USA

7 SOFTWARE: FastSEQ for Windows Version 4.0

7 TYPE: DRT

7 TYPE: DRT

7 TYPE: DRT

7 CRANISM: homo sapiens

Query Match 100.0%; Score 2500; DB 14; Length 479; Best Local Similarity 100.0%; Pred. No. 1.3e-222; Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps

1 MDATIAPHRIPPEMPQYGEENHIFELMQNMLEQLLIHQPEDPIPFMIQHLHRDNDNVPRI

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121 LIQERLABEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVLIBRNLGKRI 180

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sequence 2, Application US/10798773
; Sequence 2, Application US/10798773
; Publication No. US20050019885A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Xie, Qiongshu
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; TITLE OF INVENTION: NUMBER: US/10/798,773
; CURRENT APPLICATION NUMBER: US/10/141,634
; PRIOR APPLICATION NUMBER: US/10/141,634
; PRIOR PILING DATE: 2001-05-09
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEC ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2.
; LENARTH 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 SADQPCVDVFYQALTXVQSNHRTNAPFTPRVLLLGPVGSGKSLQAALLAQKYRLVNVCCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VILGPPASGKTTIAMMLCKHINSSLLTLENLILMEFSYTATEARRLYLQRKTVPSALLVQ 120
                                                                                                                                                                                                                           QAHLLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
                                                                                                                                                                                                                                                                                 VILGPPASGKTTIAMMLCKHLNSSLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQ 120
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                                                                                                                                                                                                         QLLKEAVADRTTFGELIQPFFEKEMAVPDSLLMKVLSQRLDQQDCIQKGWVLHGVPRDLD
                                                                                                       181 DPQTGBIXHTTFDWPPESBIQNRLMVPEDISELETAQKLLEYHRNIVRVIPSYPKILKVI
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Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 479; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: homo sapiens
US-10-798-773-2
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TYPE: PRT
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                                                                                                                                     QLLKEAVADRTTFGELIQPFFEKEMAVPDSLLMKVLSQRLDQQDCIQKGWVLHGVPRDLD 360
                                                                                                                                                                                                                                    QAHLLNRLGYNPNRVPFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
                                                                                                                                                                                                                                                     240
                                                                                                                   300
                                                                                                                                                                                           NPKDAEEQVKLKMDLFYRNSADLEQLYGSAITLNGDQDFYTVFEYIESGIINPLPKKIP 479
                                                                                                                                                                                                                                                                                                             1 MDATIAPHRIPPEMPQYGEENHIFELMQNMLEQLLIHQPEDPIPFMIQHLHRDNDNVPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                           SADOPCVDVFYQALTYVQSNHRTNAPFTPRVLLLGPVGSGKSLQAALLAQKYRLVNVCCG
                                                         DPQTGEIXHTTFDWPPESEIQNRLMVPEDISELETAQKLLEYHRNIVRVIPSYPKILKVI
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Best Local Similarity 100.0%; Pred. No. 1.36-222;
Matches 479; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: INJURA, KEIICHI
APPLICANT: IRIE, KYOTARO
APPLICANT: IRIE, KYOTARO
APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOWU
APPLICANT: YOSHIKAWA, TSUTOWU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KONJEL FULL-LENGTH CDNA
FITIE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALCHIN VET. 2.1
SOFTWARE: PALCHIN VET. 2.1
SENGTH: 479
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3020, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUGIYAN, TOMOYASU
OTSUKI, TETSUJI
WAKAMATUSI, AI
SATO, HIROYUKI
ISHI, SHIZUKO
YAMAMOYO, JUN-ICHI
ISONO, YUUKO
HIO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Homo sapiens
US-10-094-749-3020
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| APPLICANT: KIAH, Farrah A. |
| APPLICANT: KIAH, Farrah A. |
| APPLICANT: KIAH, Farrah A. |
| APPLICANT: AZIMZAL, Yalda |
| APPLICANT: AZIMZAL, Yalda |
| APPLICANT: AZIMZAL, Yalda |
| APPLICANT: POLICKY, Jennifer L. |
| APPLICANT: GRITHER, Megan |
| APPLICANT: GRITHER, Sajeav |
| APPLICANT: BATRA, Sajeav |
| APPLICANT: BATRA, Sajeav |
| TITLE OF INVENTION: HUMAN KINASES |
| TILE OF INVENTION: PL-0125 PCT |
| CURRENT APPLICATION NUMBER: US/10/311,034 |
| CURRENT APPLICATION NUMBER: 60/212,073; 60/215,651; 60/216,605; 60/218,372, 60/228,056 |
| PRIOR APPLICANION NUMBER: 60/212,073; 2000-06-33; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-0
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"NAMB/KEY: misc feature

"OTHER INFORMATION: Incyte ID No. US20040023242A1 621293CD1
US-10-311-034-22
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FRIBOULEY, Catherine M.
CHAWLA, Narinder K.
YAO, Monique G.
Li, Dyung Aina M.
GREENWALD, Sara R.
RAMKUMAR, Jayalaxmi
GRIFFIN Jennifer A.
KEARNEY, Liann
BURFORD, Neil
NGUYEN, Danniel B.
TANG, Y. Tom
TANG, Y. Tom
TANG, Y. Tom
TANG, Y. Tom
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ARVIZU, Chandra S.
GURURAJAN, Rajagopal
LO, Terence P.
                                                                                                                                                                                                                                                                                                                                                                                                                                             HE, Ann
THORNTON, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 25
LENGTH: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                        205 MVPEDISELETAQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQSNHRTN 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-104-047-3627

Sequence 3627, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:

TITLE OF INVENTION: No. US20030236392A1e1

TITLE OF INVENTION: No. US20030236392A1e1

TITLE OF INVENTION: No. US20030236392A1e1

TITLE OF INVENT PAPLICATION

TITLE OF INVENT APPLICATION

CURRENT PILING DATE: 2002-03-25

RAIOR APPLICATION NUMBER: US/10/104,047

SOFTHARE: PARTE: PARTE: 2002-03-25

NUMBER OF SEQ ID NOS: 4096

SOFTHARE: PARTE: PARTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 QLYGSAITLANGDQDPYTVFEYIESGIINDLPKKIP 275
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18-10-311-034-25
1 Sequence 25, Application US/10311034
2 Publication No US20040023242A1
3 PAPLICANT: VUE, Henry
APPLICANT: VUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: AND YOUNG, Janice
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; ORGANISM: Homo sapiens
US-10-104-047-3627
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267 FTPRVILLGBVGSGKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGELIQPFFEKEWA 326
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                                                                                                                                                                                                                                                                                                                                                      FRATURE:
NAME/KEY: SITE
LOCATION: (228)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (234); LOCATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-868-870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 PEDISELETAQKILEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQSNHRTNAP 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 QALRIQILGITPRHVIVLSAPDTVLIERNIGKRIDPQTGEIYHTTFDWPPESBIQNRLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                generic 868, Application US/09764868
; Sequence 868, Application Solution
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: NUMBER: US/09/764,868
; CURRENT PEPLICATION NUMBER: US/09/764,868
; CURRENT PILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT232 CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17 Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 46.6%; Score 1166; DB 9; Length 236; Best Local Similarity 100.0%; Pred. No. 2e-99; Matches 225; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 VPDSILIMKVI.SQRLDQQDCIQKGWVLHGVPRDLDQAHLIMRIGYN 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
22.1%; Score 553; DB 9; L
Best Local Similarity 100.0%; Pred. No. 4.2e-43;
Matches 106; Conservative 0; Mismatches 0;
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US-09-764-868-868
                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                           LENGTH: 236
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                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Chun, Miyoung
APPLICANT: Chun, Miyoung
APPLICANT: Chun, Miyoung
APPLICANT: Rapeller-Libermann, Rotale Racelel R.
APPLICANT: Rapeller-Libermann, Rotale R.
TITLE OF INVENTION: No. US20030092116Alel Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Pregnentation Factor-Like, Phosphatidylesrine Synthase-Like, DNA
TITLE OF INVENTION: Pregnentation Factor-Like, Phosphatidylesrine Synthase-Like Molecules and Uses Therefor
TITLE OF INVENTION: and APPase-Like Molecules and Uses Therefor
TITLE OF INVENTION: and APPase-Like Molecules and Uses Therefor
TITLE OF INVENTION: and APPase-Like Molecules and Uses Therefor
TITLE OF INVENTION: 1002-06-07
FILE SEPERATOR NUMBER: 05/190,179
PRIOR PELING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 05/195,946
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 05/195,946
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 05/195,947
PRIOR APPLICATION NUMBER: 05/195,949
PRIOR PILING DATE: 2000-02-29
PRIOR PILING DATE: 2000-02-29
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-21
PRIOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAMMICKHINSSLITLENLILNEFSYTATEARRLYLORKTVFSALLVOLIOBRLABEDCI
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                                                         Sequence 22, Application US/10165800 Publication No. US20030092116A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-10-165-800-22
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US-09-764-868-870 ; Sequence 870, Application US/09764868 ; Patent No. US20020168711A1

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Sequence 268668 Application US/10424599
Publication No. US20040031072A1
Publication No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 268668
                                                                APPLICANT: Xie, Giongshu
APPLICANT: Abuin, Alejandro
APPLICANT: Abuin, Alejandro
APPLICANT: Abuin, Alejandro
APPLICANT: Abuin, Alejandro
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX.0344-USA
CURRENT PELING DATE: 2004-03-11
PRIOR APPLICATION WUMBER: US/10/141,634
PRIOR APPLICATION WUMBER: US/00/141,634
PRIOR APPLICATION WUMBER: US 60/289,727
PRIOR FILING DATE: 2001-05-09
RIOR FILING DATE: 2001-05-09
SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 GKSLQAALLAQKYRLVNVCCGQLLKEAVADRTTFGBLIQPFFBKEMAVPDSLLMKVLSQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 94; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_8462C.1.pep
US-10-424-599-268668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 LYGSAITLNGDQDPYTVFEYIESGIINPLPKKIP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LYGSAITLAGDQDPYTVFEYIESGIINPLPKKIP 94
Publication No. US20050019885A1
                  GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
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APPLICANT: Xie, Qiongshu
APPLICANT: Xie, Qiongshu
APPLICANT: Xie, Qiongshu
APPLICANT: Abun, Alejandro
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: NO. US20030008365Alel Human Kinases and Polynucleotides Encoding
FILE REPERENCE: LEX-0344-USA
CURRENT APPLICATION NUMBER: US 60/289,727
PRIOR PPLICATION NUMBER: US 60/289,727
PRIOR PILING DATE: 2002-05-09
NUMBER OF SEQ ID NOS: 4
SSETWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 94
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                                                                     Sequence 1179, Application US/09764868

Fatent No. USZO02068711A1

GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232

CURRENT PILING DATE: 2001-01-17

FILE OF INFORMATION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232

CURRENT PILING DATE: 2001-01-17

FILOT application data removed - refer to FALM or file wrapper
NUMBER OF SEQ ID NOS: 1510

SEQ ID NO 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 19.6%; Score 491; DB 14; Length 94; l Similarity 100.0%; Pred. No. 1.8e-37; 94; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.1%; Score 553; DB 9; I
Best Local Similarity 100.0%; Pred. No. 4.2e-43;
Matches 106; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4, Application US/10141634; Publication No. US20030008365A1; GENERAL INFORMATION:
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US-10-798-773-4
; Sequence 4, Application US/10798773
                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-764-868-1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: homo sapiens
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Best Local S
Matches 94
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Labaska, Jack E
APPLICANT: Labaska, Jack E
APPLICANT: Sallo Involic C
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
FILE REPERENCE: 38-21(53313) B
FILE REPERENCE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 GSDNGKRAKQYMEKGQLVPDEIVVMVKERLLKPDSKENGWLLDGYPRSLSQATALEALG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 YNENRVFFINVPFDSIMERLTLRRIDPYTGERYHLMYKPPFTMEIOARLLONFKDAEEOV 429
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14.5%; Score 363.5; DB 15; Length 303;
Best Local Similarity 37.3%; Pred. No. 6.66-25;
Matches 78; Conservative 40; Mismatches 90; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 KLKMDLFYRNSADLEQLYGS-AITINGDQDPYTVFEYIESGIINPLPKK 477
                                                                                                                                                                                                                                                                                                                                                                 Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                       89; Indels
                                                                                                                                                                                                                                                                       ; FEATURE:
1. OTHER INFORMATION: Clone ID: PAT_MRT3847_14959C.1.pep
US.10-424-599-191515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Clone ID: LIB3060-027-G7_FLI.pep
US-10-425-114-47870
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 34.5%; Pred. No. 9.8e-26;
Matches 79; Conservative 45; Mismatches 89;
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF EQ ID NOS: 285684
SEQ ID NO 191115
LENGTH: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-425-114-47870
US-10-425-114-47870
Sequence 47870, Application US/10425114
Publication No. US/20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                      ORGANISM: Glycine max
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ORGANISM: Zea mays
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APPLICANT: Kovalid, David K.
APPLICANT: Kovalid, David K.
APPLICANT: Kovalid, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barba
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; Sequence 191515, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
; APPLICANT: Zhou Yihua
; APPLICANT: Zoo Yongwei
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                      211 KIYHLKFFPPDTEEIKARLITRPDDTEEKVKSRLNIYKQNAEAASSSY-SSITHKIDGSH 269
                                                        ERYHLMYKPPPTMEIGARLLONPKDAEEQVKLKMDLFYRNSADLEQLYGSAIT--LNGDQ 457
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14.9%; Score 372.5; DB 16; Length
Best Local Similarity 34.3%; Pred. No. 9e-26;
Matches 86; Conservative 41; Mismatches 99; Indels
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                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-437-963-120944
US-10-437-963-120944, Application US/10437963
; Sequence 120944, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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268 ILVKVQGDATVDAVFAKIDELLGSILEKK 296 දු පු

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	in the state of th	Segmence 1 Appli	Semience 1301 An	Segmence 17 April	Semionor 1617	Segmence 1637, Ap	Sequence 21, Appl	Sequence 23/, App	Today of the State	Sometice 23/, App	Sequence 23, Appl	W'/ocor apprended
Q.I	US-10-141-634-1	US-10-798-773-1	US-10-094-749-1381	US-10-478-146-17	US-10-104-047-1657	US-10-165-800-21	US-09-764-868-257	US-10-311-034-51	US-10-098-841-257	TIS-10-165-800-23	US-09-918-995-16667	
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10 US-09-918-995-29164 Sequence 255, App 9 US-09-764-868-255 Sequence 255, App 14 US-10-14-654-3 Sequence 3, Appliance 18-10-798-773-3 Sequence 3, Appliance 18-10-798-773-3 Sequence 3, Appliance 18-10-029-386-19439 Sequence 19439, Appliance 18-10-029-386-19439 Sequence 19439, Appliance 18-10-425-115-16-16-16-16-16-16-16-16-16-16-16-16-16-	US-10-282-1224-13434 Sequence US-10-276-211847 Sequence US-10-276-32-10112 Sequence US-10-276-32-10112 Sequence US-10-282-1213-185038 Sequence US-10-282-1224-185038 Sequence US-10-282-1224-1844 Sequence US-10-282-1224-1844 Sequence US-10-282-1224-1855 Sequence	ALIC 0141634 5A1 0030008365 A US/10/141 05-08 5 60/289,7	100.0%; Score 1440; DB 14; Length 1440; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ATGGACGCCACTATCGCCCCGCACGTATCCCCCCGAGATGCCCCAGTACGGGGAGGGG 60
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36.6 322 3222 1322 134.85 13.6 92.8 87.8 87.8 87.8 87.4 87.4 85.4 85.4 85.4 87.4 87.4 87.4 87.4 87.4 87.4 87.4 87	69 68 68 68 69 68 68 68 68 68 68 68 68 68 68 68 68 68	SULT 1 -10-141-634-1 Figure 1. Application US/10141634 Publication No. US20030008365A1 Publication No. US20030008365A1 APPLICANT: Yu, Kuanchuan APPLICANT: Yu, Kuanchuan APPLICANT: Xie, Qiongshu APPLICANT: Abuin, Alejandro APPLICANTON: No. US200300083 TITLE OF INVENTION: No. US200300083 TITLE OF INVENTION: No. US200300083 THER REPERENCE: LEX-034-USA CURRENT FILING DATE: 2002-05-09 PRIOR FILING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 4 -05-09 NUMBER OF SEQ ID NOS: 4 -05-09 NUMBER OF SEQ ID NOS: 4 -05-09 TYPE: DNA ORGANISM: homo sapiens -10-141-634-1	SO C
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TYPE: DNA ORGANISM: Homo sapiens
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                               CAGAACCGTCTCATGGTGCCAGAGGACATCTCAGAGGCTGGAGACGGCTCAGAAACTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10478146
Sequence 17, Application US/10478146
Sequence 17, DS20040203097A1
GENERAL INFORMATION:
APPLICANT: INCYTE CRPORATION; YUE, Henry;
APPLICANT: LU, Dyung Aina M.; AZIMAAI, Yalda;
APPLICANT: DIG, Li; LEE, Ernestine A.;
APPLICANT: HAFALIA, April J.A.; BECHA, Shanya D.;
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APPLICANT: TANG, Y. Tom; LAL, Preeti G.;
APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;
APPLICANT: RAMKUNAR, Jayalaxmi; ELLIOTT, Vicki S.;
APPLICANT: RANKINARAR, Anita; DUGGAN, Brendan M.;
APPLICANT: RANKINARAR, Anita; DUGGAN, Brendan M.;
APPLICANT: TRAN, Uyen K.; CHAMLA, Narindar K.;
APPLICANT: GANDHI, Ameena R.; YAO, Monique G.;
APPLICANT: GANDHI, Ameena R.; YAO, Monique G.;
APPLICANT: GANDHI, Ameena R.; YAO, Monique G.;
APPLICANT: GROWSKY, Mark L.; ZEBARJADIAN, Yeganeh;
APPLICANT: BOROWSKY, Mark L.; ZEBARJADIAN, Yeganeh;
APPLICANT: BOROWSKY, Mark L.; ZEBARJADIAN, Yeganeh;
APPLICANT: BOROWSKY, Mark L.; ZEBARJADIAN, Yeganeh;
APPLICANT: GLIEN, David; JIN, Pei
TITLE OF INVENTION: KINASES AND PHOSPHATASES
FILE REFERENCE: PF-095 USN
CURRENT APPLICATION NUMBER: US 60/293,665
PRIOR FILING DATE: 2001-05-24
PRIOR PELING DATE: 2001-05-24
PRIOR PELING DATE: 2001-07-06
PRIOR PELING DATE: 2001-07-07
PRIOR PELING DATE: 2001-07
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches
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OTHER INFORMATION: Incyte ID No: 72063274CB1
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S-10-104-04/ Sequence 16 Sequence 16 Sequence 16 Sepublication CERNEAL INE APPLICANTA TITLE OF 1 FILE REFER CURRENT AF CURRENT AF CURRENT AF PRIOR FILE SEQ ID NO 1 LENGTH: DNA COFFRANTSN: SOFTWARE: SOFTWARE	Db   448   GTGGTGACATCTGTATCTGCTCTCATGGCTGGATGGCATCCCTGAGACGCGTG   507
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Pred. No. 0;
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PRIOR APPLICATION NUMBER: 60/186,234
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/781,677
PRIOR PILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.06
SEQ ID NO 21
LENGTH: 1452
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Best Local Similarity 86.5%;
Matches 1246; Conservative (
                                                                                                                                                                                                               , NAME/KEY: CDS
; LOCATION: (219)...(995)
US-10-165-800-21
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APPLICANT: Chun, Miyoung
APPLICANT: Gluckmann, Maria Alexandra
APPLICANT: Gluckmann, Maria Alexandra
APPLICANT: Gluckmann, Maria Alexandra
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Mayers, Rachel Er.
TITLE OF INVENTION: No. US20030092116Alel Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Pageneration Pactor-Like, Phosphatidylserine Synthase-Like,
TITLE OF INVENTION: and APPRSe-Like Molecules and Uses Therefor
TITLE OF INVENTION: and APPRSe-Like Molecules and Uses Therefor
TITLE OF INVENTION: and APPRSe-Like Molecules and Uses Therefor
TITLE OF INVENTION: and APPRSe-Like Molecules and Uses Therefor
TITLE OF INVENTION: and APPRSe-Like Molecules and Uses Therefor
TITLE OF INVENTION: 0001-02-02
PRIOR APPLICATION NUMBER: 09/790,179.
PRIOR APPLICATION NUMBER: 60/185,946
PRIOR FILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/790,180
PRIOR PILING DATE: 2000-02-29
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                                                                                                                                                                                                          Length 1223;
                                                                                                                                                                                                  Query Match 71.4%; Score 1027.6; DB 9; Length Best Local Similarity 95.6%; Pred. No. 0; Matches 1153; Conservative 0; Mismatches 10; Indels
         i LOCATION: (1181)
i OTHER INPORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1191)
i OTHER INPORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1193)
i OTHER INPORMATION: n equals a,t,g, or c
NAME/KEY: SITE
loCATION: (1293)
i OTHER INPORMATION: n equals a,t,g, or c
NAME/KEY: SITE
loCATION: (1203)
i OTHER INPORMATION: n equals a,t,g, or c
loCATION: (1218)
i OTHER INPORMATION: n equals a,t,g, or c
loCATION: (1218)
i OTHER INPORMATION: n equals a,t,g, or c
loCATION: (1208)
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                                                           841 AAAAGICTGCAGGCCGCCTCCTGGCCCAGAAATACAGGCTTGTCAATGTCTGGTGGG
                                                                                          CAACTGCTGAAAGAGGCTGTGGCAGATAGGACCACGTTTGGCGAGCTCATCCAGCCCTTC
                                                                                                                                                        979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ## Sequence 257, Application US/09764868
## Patent No. US20020168711A1
## Patent No. US20020168711A1
## APPLICANT: Rosen et al.
## TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
## CURRENT APPLICATION NUMBER: US/09/764,868
## CURRENT APPLICATION NUMBER: US/09/764,868
## Prior application data removed - refer to PALM or file wrapper
## NUMBER OF SEQ ID NOS: 1510
## SOFTWARE: PatentIn Ver. 2.0
## SEQ ID NO 257
## LENGTH: 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
PRAYURS:
NAME/KEY: SITE
LOCATION: (78)
OTHER INPORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (307)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1163)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1163)
OTHER INFORMATION: n equals a,t,g, or c
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FILE REPERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
CURRENT FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-08-
RIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-08-
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL PROGRAM
SEQ ID NO 51
LENGTH: 995
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                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                 Length 995;
                                                                                                                                                                                                                                                                                                     , NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 621293CB1
US-10-311-034-51
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                               Query Match
60.3%; Score 868; DB 17; 1
Best Local Similarity 100.0%; Pred. No. 1.5e-269;
Matches 868; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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                 CTGGCCCAGAAATACAGGCTTGTCAATGTCTGCTGTGGGCAACTGCTGAAAGAGGCTGTG
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Sequence 51, Application US/10311034
Publication No. US20040023242A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: INC. Preet.i
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: GANDHI, Amena R.
APPLICANT: CHAMLA, Narince
APPLICANT: CHAMLA, Narince K.
APPLICANT: CHAMLA, Narince K.
APPLICANT: YAO, Monique G.
APPLICANT: TANG, Monique G.
APPLICANT: TANG, Monique G.
APPLICANT: GREENWALD, Sara R.
APPLICANT: GREENWALD, Sara R.
APPLICANT: GREENWALD, Saria R.
APPLICANT: GREENWALD, Sanial B.
APPLICANT: GREENWALD, Sanial B.
APPLICANT: GREENWALD, Sanial B.
APPLICANT: TANG, Y. Tom
APPLICANT: HAFALIA, Mariah R.
APPLICANT: THORYTON, Mariah R.
APPLICANT: HAFALIA, April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HE, Ann
THORNTON, Michael
HAFALIA, April
ARVIZU, Chandra S.
GURURAJAN, Rajagopal
LO, Terence P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHAH, FARTAN A.
RECIPON, Shirley A.
AZIMZAI, Yalda
POLICKY, Jennifer L.
DING, Li
GRETHER, Megan
ELLIOTT, VICK! S.
THANGANELU, Kavitha
BATRA, Sajeev
ISON, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1161 GCGGCT 1166
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Sequence 23, Application US/10165800

Publication No. US20030092116A1

GENERAL INFORMATION

APPLICANT: Chun, Miyoung

APPLICANT: Chun, Miyoung

APPLICANT: Gluckmann, Maria Alexandra

APPLICANT: Gluckmann, Maria Alexandra

APPLICANT: Gluckmann, Maria Alexandra

APPLICANT: Meyers, Rachel E.

TITLE OF INVENTION: No. US20030092116A1e1 Nucleic Acid Sequences Encoding

TITLE OF INVENTION: No. US20030092116A1e1 Nucleic Acid Sequences Encoding

TITLE OF INVENTION: No. US20030092116A1e1 Nucleic Acid Sequences Encoding

TITLE OF INVENTION: And APPRASE-Like Molecules and Uses Therefor

TITLE OF INVENTION: and APPRASE-Like Molecules and Uses Therefor

TITLE OF INVENTION NUMBER: US/10/165,800

CURRENT APPLICATION NUMBER: 09/790,179

PRIOR FILING DATE: 2001-02-21

PRIOR FILING DATE: 2001-02-29

PRIOR PLICATION NUMBER: 60/185,609

PRIOR PLILOATION NUMBER: 60/185,946

PRIOR PLILOATION NUMBER: 60/185,946

PRIOR FILING DATE: 2001-02-29

PRIOR FILING DATE: 2001-02-29

PRIOR FILING DATE: 2001-02-29

PRIOR FILING DATE: 2001-02-29

PRIOR FILING DATE: 2001-02-21

PRIOR APPLICATION NUMBER: 60/185,947
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                                                507 TGGCCACCCGAATCTGAAATCCAGAACCGTCTCATGGTGCCAGAGGACATCTCAGAGGTG
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                        CTGGGGATCACCCCAGACACGTCATTGTGCTGAGTGCTCCAGACACGGTCCTGATCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386
GAAAATGGACCTGTTCTACAGGAACTCAGCTGACTTGGAGCAGTTGTATGGGTCGGCCAT 782
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                                     AATGAGTTTTCCTATACGGCCACCGAAGCCAGAAGGCTTTATCTGCAAAGGAAGAAGTT
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Agundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Ana, Yunging
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Chen, Rui-hong
APPLICANT: Anang, Jiwei
APPLICANT: Dang, Jiwei
APPLICANT: Olan, Xiachong B.
APPLICANT: Olan, Xiachong B.
APPLICANT: Olan, Siachong B.
APPLICANT: Olan, Siachong B.
APPLICANT: Olan, Siachong B.
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Siachong B.
APPLICANT: Chen, Siachong B.
APPLICANT: Olan, Siachong B.
APPLICANT: Chengham Chengham
FRICK APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 3311
SEQ ID NO 257.
LENGTH. 1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1778;
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Best Local Similarity 92.0%; Pred. No. 8.3e-235;
Matches 803; Conservative 0; Mismatches 70;
                                                                                                                 Sequence 257, Application US/10098841 Publication No. US20020197679A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (63)..(1778)
US-10-098-841-257
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Sequence 16667, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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Matches 407; Conservative
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CORGANISM: Homo sapiens
US-09-918-995-16667
        RESULT 11
US-09-918-995-16667
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                                                                                                                                                                                                  Query Match 52.8%; Score 759.8; DB 14; Length 774; Best Local Similarity 99.7%; Pred. No. 1.4e-234; Matches 761; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITGGCGAGCTCAICCAGCCTTCTTGAAAAGGAGATGGCAG 979
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/795,038
PRIOR FILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/186,234
PRIOR PILING DATE: 2000-02-29
PRIOR PILING DATE: 2001-02-21
PRIOR PILING DATE: 2001-02-21
PRIOR FILING DATE: 2000-02-10
                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                               ; ORGANISM: DOI
US-10-165-800-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647 CTCAGAAACTGCTGGAGTATCATAGGAACATCGTCAGGGTCATTCCCTTCCTACCCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                   407 ggarrenggargecarcecrgaegaegeegrgagecaecrergaggarecagaecerresga
                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 TCACACCCAGACACGTCATTGTGCTGAGTGCTCCAGACACGGTCCTGATCGAGAGAAACT
                                                                                                                                                                                                                                                                                                                                                                                 347 CGCTGCTCCACCTGATTCAGGAACGCCTGGCTGAAGAGATTGCATCAAGCAGGGCT
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US-09-29164

US-09-29164, Application US/09918995

; Publication No. US20030073623A1

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES

; TITLE REFERENCE: 2011-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT PILING DATE: 1999-01-20

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR PILICATION NUMBER: US/09/235,076

; RUGHER OF SEQ ID NOS: 38054

; SQPTWARE: FastESQ for Windows Version 3.0

; SEQ ID NO 29164
                                                                                                                                                                                                                                                                                           Length 407;
TITLE OF INVENTION: MOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: MOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 2011-756 CURRENT APPLICATION NUMBER: US/09/215,076 PRIOR PILING DATE: 1999-01-20 NUMBER OF SEQ ID NOS: 38054 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 16667
                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                       28.3%; Score 407; DB 10; I 100.0%; Pred. No. 1.4e-120; tive 0; Mismatches 0;
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GGACCTGTTCTACAGGAACTCAGCTGAACTTGGAGCAGTTGTATGGGTCGACCATCACCCT 1358
                                             1119 CAGGETGTTTTCCTGAATGTGCCATTTGATTCCATCATGGAGCGGCTGACTCTGAGAAG 1178
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                                                                                                                                                                                 RESULT 14
US-09-764-868-566

15 Sequence 566 Application US/09764868

16 Patent No. US20020168711A1

17 GENERAL INFORMATION:

17 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

18 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

19 TITLE OF INVENTION: NUMBER: US/09/764,868

10 CURRENT APPLICATION UNDER: US/09/764,868

10 CURRENT APPLICATION AGE removed - refer to PALM or file wrapper: NUMBER OF SEQ ID NOS: 1110

10 SOFTWARE: PatentIN Ver. 2.0

11 SEQ ID NO 566

12 ENGTH: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.4%; Score 322; DB 9; Length 510
Best Local Similarity 100.0%; Pred. No. 4.8e-93;
Matches 322; Conservative 0; Mismatches 0; Indels
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CTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-566
                                                                                                                           1419 CCTGCCCAAGAAATCCCCTGA 1440
                                                                                                                                           358 CCTGCCCAAGAAATCCCCTGA 379
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Publication No. US200300035531
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: SITE
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US-10-141-634-3
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                                                                                                            0; Gaps
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                                                                               Query Match 25.5%; Score 366.6; DB 10; Length 447; Best Local Similarity 97.6%; Pred. No. 1.7e-107; Matches 372; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 255, Application US/09764868
Parent No. US20020169711A1
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232 US/09/764,868
CURRENT FILING DATE: 2001-01-17
PT10T application date removed - refer to PALM or file wrapper
SOFTWARE: PatentIn NoS: 120
SOFTWARE: PatentIn Ver. 2.0
SER ID NO. 255
LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.4%; Score 322; DB 9; Length 509; Best Local Similarity 100.0%; Pred. No. 4.8e-93; Matches 322; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

; LCCATION: (1)...(447)

: OTHER INFORMATION: n = A,T,C or G

US-09-918-995-29164
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-764-868-255
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APPLICANT: Xie, Qiongshu
APPLICANT: Abuin, Alejandro
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: No. US20030008365Alel Human Kinases and Polynucleotides Encoding
FILLE REFERENCE: LEX.0344-USA
CURRENT APPLICATION NUMBER: US/10/141,634
CURRENT APPLICATION NUMBER: US 60/289,727
PRIOR FILING DATE: 2001-05-09
FRIOR FILING DATE: 2001-05-09
SOUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 285
TYPE: DNA
ORGANISM: homo sapiens
US-10-141-634-3
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19.8%; Score 285; DB 14; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.4e-81;
Matches 285; Conservative 0; Mismatches 0; Indels (
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Search completed: March 20, 2005, 01:40:30 Job time : 815 secs

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Sequence 5541, Ap
Sequence 5, Appli
Sequence 2, Appli
Sequence 3207, Appli
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Sequence 5762, Ap
Sequence 6764, Ap
Sequence 1243, Ap
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9224, Ap
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US-09-252-991A-4526
US-09-139-139A-3207
US-09-139-130A-3207
US-09-149-016-5838
US-09-149-016-5838
US-09-140-16-1243
US-09-252-991A-5544
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                                          OM nucleic - nucleic search, using sw model
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Gaps . 0

DB 4; Length 1440; 0; Indels

Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches

9 9 61 AACCACATCTTCGAGTTGATGCAGAACATGCTGGAGCAACTCCTGATCCACCAGCCCGAA 120 

1 ATGGACGCCACTATCGCCCCCGCACCGTATCCCCCCCGAGATGCCCCCAGTACGGGGAGGAG 

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121 GATCCCATCCCTTCATGATCCAGCACTTGCATAGAGACAACGACAATGTGCCCCAGGATT 180

CTGAACAGCAGTCTCCTCACCCTGGAGAACCTGATCTTAAATGAGTTTTCCTATACGGCC 241 CTGBACAGCAGTCTCCTCACCCTGGAGAACTGATCTTAAATGAGTTTTCCTATACGGCC

241

181 GTAATATTAGGTCCACCGGCCTCAGGGAAAACAACAATAGCAATGTGGCTCTGCAAACAT 240

Sequence 14297, A Sequence 1324, A Sequence 13064, A Sequence 2, Applia Sequence 1, Applia Sequence 11, Applia Sequence 5442, Applia Sequence 5433, Applia Sequence 1176, Applia Sequence 1176, Applia Sequence 1207, Applia Sequence 1217, Applia Sequence 1217, Applia Sequence 1210, Applia Sequence 1210, Applia Sequence 1210, Applia Sequence 1210, Applia Sequence 179, Applia Sequence 179, Applia Sequence 122,	and Polynucleotides Encoding the Same
US-09-949-016-14297 US-09-949-016-12224 US-09-949-016-12064 US-09-103-840A-1 US-09-252-991A-5442 US-09-252-991A-5443 US-09-902-540-584 US-09-902-540-584 US-09-902-540-1176 US-09-902-540-1176 US-09-252-991A-147 US-09-252-991A-147 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210 US-09-902-540-1210	LIGNMENTS Human Kinases 141,634 9,727 Lon 4.0
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229 330 390.2 331 330 330 330 330 330 330 330 330 330	RESULT 1 US-10-141-634-1 Sequence 1, Application Patent No. 6734010 GENERAL INPORMATION: APPLICANT: Yu, Xuanchua APPLICANT: Xie, Qiongs APPLICANT: Xie, Qiongs APPLICANT: Xie, Qiongs APPLICANT: Abuin, Ale) APPLICANT: Abuin, Ale) PILER REFERENCE: LEX-034 CURRENT APPLICATION NUMBE PRIOR PILING DATE: 2001 CURRENT PILING DATE: 2001 NUMBER OF SEQ ID NOS: 4 SOCTWARE: FASTSEQ for W SEQ ID NO 1 LENGTH: 1440 TYPES DNA
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                      ATCCCTGAGACGCGTGAGCTCTGAGGATCCAGACCCTGGGGATCACACACGACAC
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361 CIGATICAGGAACGCCIGGCIGAAGAGGAITGCAICAAGAGGCIGGAITCIGAITCIGGAIGGC
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Same
                                                      APPLICANT: YL, Kunchuan
APPLICANT: YL, Chongehu
APPLICANT: YL, Chongehu
APPLICANT: Abuin, Alejandro
APPLICANT: Walke, D. Wad
TITLE OF INVENTION: No. 6734 1001 Human Kinases and Polymucleotides Encoding the FILE REPERENCE: LEX-0344-USA
CURRENT PELLING NUMBER: US/10/141,634
CURRENT PILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/289,727
PRIOR APPLICATION NUMBER: US 60/289,727
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 3495, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; APPLICANT: Glordano, J.Y.
; TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; Patent No. 6783961
; PILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT PILING DATE: 1999-02-26
; PRIOR PILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 3495
; LENGTH: 264
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100.0%; Pred. No. 9.1e-74;
ive 0; Mismatches 0;
US-10-141-634-3
; Sequence 3, Application US/10141634
; Patent No. 6734010
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 285; Conservative
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NAME/KEY: CDS
LOCATION: 67..264
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Sequence 4328, Application US/09252991A
Batent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: MREGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT PELLIGATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PELLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
FIRENCE APPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-07-27
FIRENCE FILING DATE: 1998-07-27
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TITLE OF INVENTION: ALEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 792
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4.6%; Score 66.4; DB 4; Length 74
Best Local Similarity 49.0%; Pred. No. 3.9e-09;
Matches 206; Conservative 0; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4328
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Best Local Similarity 79.0%; Pred. No. 1.6e-22;
Matches 154; Conservative 5; Mismatches 0; Indels 36;
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LOCATION: 41
OTHER INFORMATION: Xaa=11e or Asn
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US-09-513-999C-3495
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LOCATION: 46
OTHER INFORMATION: Xaa=Leu or
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                                                     OTHER INFORMATION: n=a,
                WAME/KEY: misc_feature
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LOCATION: 222
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NAME/KEY: UNSURE
LOCATION: 51
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LOCATION: 52
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RESULT 4 US-09:252-991A-4328/c

TYPE: DNA . ORGANISM: Pseudomonas aeruginosa

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Sequence 4423, Application US/09252991A

Paternam North Companies of the Sequence Relating TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 4423
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4.6%; Score 66.4; DB 4; Length 1

Best Local Similarity 49.0%; Pred. No. 4.7e-09;

Matches 206; Conservative 0; Mismatches 211; Indels
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US-09-252-991A-4423
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48.9%; Pred. No. 2.9e-06;
tive 0; Mismatches 217; Indels
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Patent No. 6001624
GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Shah, Purvi
ITILE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0256 US
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF. TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 814 base pairs TYPE: nucleic acid STRANDENESS: single TOPOLLGY: linear IMMEDIATE SOURCE: LERRAY: COMBENSE: CLORE: CLORE: LERRAY: COMBENSE: CLORE: CLORE: CLORE: LERRAY: COMBENSE: CLORE: CLORE: LERRAY: COMBENSE: CLORE:                                                                          APPLICATION NUMBER: US/NEILING DATE: Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
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Best Local Similarity 48.98
Matches 216; Conservative
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US-09-225-366-2
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                              Sequence 5541, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
TILLS GATY Breton et. al
TILLS OF INVENTION: UNCLERIC AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TILLE OF INVENTION: UNCLERIC AND THERAPEUTICS
TILLE OF INVENTION: UNCLERIC AND THERAPEUTICS
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
SEQ ID NOS: 14342

LENGTH: 678
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Best Local Similarity 48.8%; Pred. No. 3.3e-08;
Matches 201; Conservative 0; Mismatches 208; Indels 3; Gaps
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| Patent No. 2865160
| GENERAL INFORMATION:
| APPLICANT: Hillman, Jennifer L. APPLICANT: Hillman, Jennifer L. APPLICANT: Shah, Purvi
| CORRESPONDENCE ADDRESS:
| ADDRESSES: Incyte Pharmaceuticals, Inc. |
| STREET: 3174 Porter Drive |
| STREET: 3174 Porter Drive |
| STATTS: CA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5541
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1105 GGCTACAATCCCAACAGGGTGTTTTTCCTGAATGTGCCATTTGATTCCATCATGGAGGGG 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          985 GACAGCCTCCTCATGAAGGTGCTGAGCCAGCGCCTGGACCAGCAGGACTGCATCCAGAAA 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1045 GGCTGGTGCTACACGGCGTCCCGCGGGACCTCGACCAGGCACACCTGCTGAACGCCTG 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 adcirácridarigaandarticcaadaacacrirccacadadadagacccinganad---a 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 GCTTATCAGATCGACACAGTGATTAACCTGAATGTGCCTTTGAGGTCATTAAACAACGC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 citakirectesetricateseketeseketesetetataakatrisaatreaaeteet 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 dargargicargacredecid-----geeerreargagergaaaarereaceagrar 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          925 GAIAGGACCACGITITGGCGAGCTCATCCAGCCCITCTITGAAAAGGAGAIGGCAGITCCI 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 CGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGGAAACTCATCCCA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              805 CCGAGGGTGCTGCTGCTCGGGCTGGGGAAAAGTCTGCAGGCCGCCTCCTG 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          865 GCCCAGAAATACAGGCTTGTCAATGTCTGCTGGGCAACTGCTGAAAGAGGCTGTGGCA 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 criccia decionida rearidade de ceceso de constructos de contra 
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Best Local Similarity 48.9%; Pred. No. 2.9e-06;
Matches 216; Conservative 0; Mismatches 217; Indels
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION WINGBER: 08/829,027
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0256 US
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1225 CCTCCCACCATGGAGATCCAGG 1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 854 base pairs
TYPE: nucleic acid
STRANDEDDRESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LINGARY: Consensus
CLONE: 2122022
US-09-225-366-2
                                      STREET: 31/7.
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                                                                                                                                 STATE: C
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REPERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
FARLIER APPLICATION NUMBER: PCT/US98/04493
FARLIER PILING DATE: 1998-03-06
FARLIER APPLICATION NUMBER: 60/040,162
FARLIER PILING DATE: 1997-03-07
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RAPPLICATION NUMBER: 60/047,633

RAPLICATION NUMBER: 60/047,633

RETLING DATE: 1997-05-23

REPLING DATE: 1997-05-23

REPLING DATE: 1997-05-23

REPLING DATE: 1997-05-23

RAPPLICATION NUMBER: 60/047,618

REPLING DATE: 1997-05-23

RAPPLICATION NUMBER: 60/047,503

REPLING DATE: 1997-05-23

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R APPLICATION NUMBER: 60/047,587
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,598
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,613
R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,163
R FILING DATE: 1997-03-07
R PILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,615
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APPLICATION WUMBER: 60/047,597
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,333
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/038,621
Sequence 68, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
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116 cricidadederidarearigadedeceedadereagacaaceareridedeare 175 865 GCCCAGAAATACAGGCTTGTCAATGTCTGCTGGGCAACTGCTGAAAGAGGCTGTGGCA 924 176 ACTACACACTTCGAGCTGAAGCACCTCTCCAGGGGGACCTGCTCGGGACAACATGCTG 235 925 GATAGGACCACGTTTGGCGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGGCAGTTCCT 984 236 CGGGGCACAGAAATTGGGGTGTTAGCCAAGGCTTTCATTGACCAAGGGAAACTCATCCCA 295 805 CCGAGGGTGCTGCTCGGGCCTGTGGGGAGAAAAGTCTGCAGGCCGCCCTCCTG Score 56.8; DB 3; Length 1751; Pred. No. 4.3e-06; 0; Mismatches 217; Indels 9 BARLIER APPLICATION NUMBER: 60/047,588
BARLIER APPLICATION NUMBER: 60/047,585
BARLIER APPLICATION NUMBER: 60/047,586
BARLIER APPLICATION NUMBER: 60/047,590
BARLIER PILING DATE: 1997-05-23
BARLIER APPLICATION NUMBER: 60/047,599
BARLIER APPLICATION NUMBER: 60/047,599
BARLIER PILING DATE: 1997-05-23
BARLIER APPLICATION NUMBER: 60/043,579
BARLIER PILING DATE: 1997-05-23
BARLIER APPLICATION NUMBER: 60/043,579
BARLIER PILING DATE: 1997-05-23
BARLIER APPLICATION NUMBER: 60/043,579
BARLIER PILING DATE: 1997-05-23
BARLIER APPLICATION NUMBER: 60/043,576
BARLIER APPLICATION NUMBER: 60/043,576
BARLIER PILING DATE: 1997-06-23
BARLIER PILING DATE: 1997-06-23
BARLIER PILING DATE: 1997-06-23
BARLIER PILING DATE: 1997-06-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DA R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,588

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,585

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,585

R RILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,586 EARLIER FILING DATE: 1997-06-13 EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-10-02 Query Match 3.9%; Best Local Similarity 48.9%; Matches 216; Conservative g .8 g 8

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-04-17
PRIOR PRILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR SECITOR NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SECITOR NUMBER: 60/231,498
NUMBER OF SECITOR NUMBER: 60/231,498
NUMBER OF SECITOR NUMBER: 60/231,498
SECITOR OF SECITOR NUMBER: 60/231,498
NUMBER OF SECITOR NUMBER: 60/231,498
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| Sequence 2, Application US/09103840A |
| Patent No. 6294328 |
| GENERAL INVORMATION: |
| APPLICANT: FLEISCHMAN, Robert D. |
| APPLICANT: WHITE, Owen R. |
| APPLICANT: WHITE, Owen R. |
| APPLICANT: WHYER, John C. |
| TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM ITLE OF INVENTION: US/09/103,840A |
| TITLE OF INVENTION: 1998-06-24 |
| URRENT APPLICATION NUMBER: US/09/103,840A |
| CURRENT FILING DATE: 1998-06-24 |
| NUMBER OF SEQ ID NOS: 2 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 2 |
| LENGTH: 4403765 |
| TITLE OF INVENTION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1102 CTGGGCTACAATCCCAACAGGGTGTTTTTCCTGAATGTGCCATTTGATTCCATCATGAG 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       862 CTGGCCCAGAAATACAGGCTTGTCAATGTCTGGTGTGGGCAACTGGTGAAAGAAGGCTGTG 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 Arcerecididaenarecracecenerecentes arcerecentes arcerecentes arcerecentes are
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2.9%; Score 41.8; DB 4; Length 2237;
Best Local Similarity 44.7%; Pred. No. 0.13;
Matches 163; Conservative 0; Mismatches 202; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1162 CGGCT 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
; ORGANISM: Human
US-09-949-016-5838
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Sequence 3207, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

CURRENT FILING DATE: 2709-2004001

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 3207

LEMANT. 1067
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                                                                                                                          .045 GGCTGGGTGCTACACGGCGTCCCGGGACCTCGACCACCACCACCTGCTGAACCGCCTG 1104
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US-09-489-039A-3207
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TYPE: DNA ORGANISM: Mycobacterium tuberculosis

Sequence 5838, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al.

US-09-949-016-5838

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us-10-798-773-1.rni

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828361 CGAGAAGCTCGGGAATCCCGCAGATCTCCACCGACACTTCCGGCGCAACATCGAAGA 828420
                                                                                                                                                                                                    828301 GAGAGITTTGTTGTTGGGACGCCCGGGGCGACAAGGGGACGCAGGCGGTGAAGCTGGC 828360
                                                                                                                                                                                                                                                                                                                                           826182 cadabagcrcasdarcccacharctrchccasachtrcrrcagasacharcahdh 826241
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                                                                                                                                                                                                                                          867 CCAGAAATACAGGCTTGTCAATGTCTGTGGGCAACTGCTGAAAGAGGCTGTGGGAA 926
                                                                                                                                                                807 GAGGGTGCTGCTCGGGCCTGTGGGCAGTGGGAAAAGTCTGCAGGCCGCCCTCCTGGC 866
                                                                                                                                                                                                                                                                                                                    927 TAGGACCACGTTTGGCGAGCTCATCCAGCCCTTCTTGAAAAGAGAGATGGCAGTTCCTGA 986
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Pred. No. 25;
0; Mismatches 116; Indels 0;
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OGASIZM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                        Query Match 2.8%;
Best Local Similarity 48.7%;
Matches 110; Conservative
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US-09-103-840A-1
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Search completed: March 19, 2005, 23:53:51 Job time: 293 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	FIGURE CONTRACTOR CONT										-		-				BU683145 III - CR - EC1						• • •	• • •
SUMMARIES	,	TD.	BC037402	AK004439	BM920443	CD515464	BI819382	BM926674	BI829572	BI767614	BI828586	CV030269	BU617945	B0016312	BY704667	BP368808	BP347783	AW069362	BU683145	AI591934	CK476676	BQ942240	CK594922	CK653506	CK470906	CK468902
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de	Query	Marci.	71.2	63.4	63.3	55.9	54.4	51.6	50.2	48.8	46.5	45.6	41.0	38.0	36.0	35.7	35.7	32.2	32.2	31.1	30.7	29.3	29.0	28.7	28.4	28.0
	0.00	21000	1025.4	912.8	911.8	805.6	783.2	743.6	723.2	703	670	656	591	547	518.4	514.2	513.8	463	463	448	441.6	422.4	417.6	413.8	408.6	403
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2 (bases 1 to 2567)
Strausberg, R.
Direct Submission
Submitted (04-SEP-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.

REMARK COMMENT

JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL

CK595309 AGENCOURT AI826091 AI826091 BR4659787 BF4659787 CCB56290 CCB574665 BW983192 CCB274665 BW983192 CCB274665 BW983192 CCB274665 BW983192 CCB274665 BW983192 CCB274665 BW983192 CCB274666 BW983192 CCB2744 AI361512 AM66381 AI361512 AM66381 AI361512 AM66381 AI362274 AI362715 BW954715 BW954715 BW742486 BW742486	BC037402  BC037402  BC037402  Sefor by mRNA linear HTC 25-WAR-2004 IMAGE:S163904), with apparent retained intron.  MGGE:S163904), with apparent retained intron.  BC037402  BC0374  BC037402  BC0374  BC037402  BC0374  BC037402	al analysis of more than 15,000 full-length sequences 1. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 52 Row: i Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction
This clone has the following problem: retained intron.
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DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
A.N., Gibbs, R.A.
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/tissue type="Brain, adult n/clone_lib="NH MGC_119"
/lab host="DH10B"
/note="Vector: pCWV-SPORT6"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 1439; Conserv
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Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Submistalon
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similar to CDNA FLJ32704 FIS, CLONE TESTI2000591, WEAKLY
SIMILAR TO ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3)
(Homo sapiens) (SPTR|Q96MA6, evidence: FASTY, 75.5%ID,
99.7%length, match=1433)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Nalveis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Nature 420, 563-573 (2002)

B of (Dasse I to 1559)

S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carminci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Harai, A., Hayatsu, N., Hiramoco, K., Hanagaki, T., Harai, Y., Itoh, M., Izawa, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, R., Salto, R., Salto, R., Salto, P., Sa
2322
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AK004439 I GI:12835623

HTC; CAP trapper.
                                                                                                                                 GCCATCACCTCAATGGGGACCAGGACCCATACAGTCTTCGAATACATCGAGGGGG 1407
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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The FANTOM Consortium and the RIKEN Genome Exploration Research
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Punctional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99Z79553
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:5750412"
/lab host="DH108"
/clone=lib="NIH MGC 122"
/lone=lib="NIH MGC 122"
/lone=lorgan: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled" lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled" lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled" lung, 16 week female
spleen; and 20-22 week male spleens. Library is oligo-dr
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                   LEW HOMO Saplens

Elkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Elkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

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String Mammalia; Fundes; Catarrhini; Hominidae; Homo.

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Tassue Procurement: Life Technologies, Inc.

Contact: Robert Strayed by: The I.M.A.G.E. Consortium (LLNL)

CONA Library Preparation: Life Technologies, Inc.

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_6709485 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750412
GATCCCATCATCATGATCCAGCACTTGCATAGAGACAACGACAATGTGCCCAGGATT
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63.3%; Score 911.8; DB 5;
Best Local Similarity 96.0%; Pred. No. 2.7e-232;
Matches 1021; Conservative 0; Mismatches 32;
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                      ACCGAAGCCAGAAGGCTTTATCTGCAAAGGAAGACAGTTCCCAGCGCGCTGCTCCTCCAG
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CD515464.1 GI:31447182
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// Organism="Homo sapiens"
// wol_type="mRNA"
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// wol_type="mNA"
// wol_type="mIAGE:10407307"
// tissue_type="mIAGE:1047307"
// tissue_type="mIAGE:104700"
// tissue_type="mIAGE:104700"
// abc_host="DHIOB-TON A (TI and TS phage resistances)"
// abc_host="PHIOB-TON A (TI and TS phage resistances)"
// abc_host="DHIOB-TON 
// abc_host=" National Cancer Institute / NIH
Bldg. 31 RmloAd7 Bethesda, MD 20892
Enail: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM488 row: h column: 04
High quality sequence stop: 759. CTGATTCAGGAACGCCTGGCTGAAGAGGATTGCATCAAGCAGGCTGGATTCTGGATGGC 420 18 ATGGACGCCACTATCGCCCCCCATACCCCCCCGAGATGCCCCCAGTACGGGGAGGAG 181 GTAATATTAGGTCCACCCCCCTCAGGGAAAACAACAATAGCAATGTGGCGTCTGCAAACAT 241 CTGAACAGCAGTCTCCTCACCCTGGAGAACCTGATCTTAAATGAGTTTTCCTATACGGCC 1 ATGGACGCCACTATOGCCCCGCACCGTATCCCCCCCGGAGTGCCCCAGTACGGGGAGGGG GATCCCATCCCTTCATGATCCAGCACTTGCATAGAGACAACGACAATGTGCCCAGGATT 421 ATCCCTGAGACGCGTGAGCAGGCTCTGAGGATCCAGACCCTGGGGATCACACCAGACAC GACCCTCAAACTGGAGAGATTTATCACACCACCTTTGACTGGCCACCCGAATCTGAAATC GTCATTGTGCTGAGTGCTCCAGACACGGTCCTGATCGAGAAACTTGGGGAAGAATC 3, Query Match 55.9%; Score 805.6; DB 6; Length 886; Best Local Similarity 98.6%; Pred. No. 6.3e-204; Matches 824; Conservative 0; Mismatches 9; Indels 3

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1130 bp mRNA linear EST 12-MAR-2002 AGENCOURT 6644707 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5767090 5', mRNA Sequence.
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11 (bases 1 to 1130)
12 (bases 1 to 1130)
13 (bases 1 to 1130)
14 (bases 1 to 1130)
15 (bases 1 to 1130)
16 (bases 1 to 1130)
17 (bases 1 to 1130)
18 (bases 1 to 1130)
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                                                                                          GTAATATTAGGCCCCCCCCCCGGGAAAACAACAATAGCAATGGGGCTCTGCAACAT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 890)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
L Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Location/Qualifiers
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                                                               GAGTATCATAGGAACATCGTCAGGGTCATTCCCTTCCTACCCCAAAATCCTCAAAGTCATC
                                                                                                                                                                 CATCGTACTAATGCCCCGGTT---CACCCGAGGGTGCTGCTGCTCGGGCCTGTGGG 833
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llarity 98.0%; Pred. No. 6.2e-198;
Conservative 0; Mismatches 13;
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Homo sapiens
                                                                                                                                                                                                                                                                                             mRNA sequence.
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Best Local Similarity
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//molltype="mRNA"
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Mammala; Butharia; Primates; Catarrhini; Hominidae; Homo.

En (bases 1 to 827)

Si NiH-MGC http://mgc.nci.nih.gov/.

Nitional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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Email: cgapbs-r@mail.nih.gov

Contact: Robert Strauberg, Ph.D.
DNA Library Preparation: Life Technologies, Inc.

CONM Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyt Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: Llanlingov

Plate: Llanlingov

High quality sequence stop: 819.
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B1829572 1 GI:15941122
EST.
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                                                                           GTCATTCCCTCCTACCCCAAAATCCTCAAAGTCATCAGTGCTGACCAGCC--ATGTGTGG
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                                                                                                                                                GACATCTCAGAGCTGGAGACGGCTCAGAAACTGCTGGAGTATCATAGGAACATCGTCAGG
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Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: The I.M.A.G.B. Consortium (LLML)

Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Robert LLMAN1284 row: m column: 11

High quality sequence stop: 682.
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/organism="Homo sapiens"
/organism="Momo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="INAGE:5210003"
/lab host="DH108"
/clone lib="NIH MGC 122"
/lone="organ: pooled lung and spleen; Vector: pCMV-SPORT6; /note="organ: pooled lung and spleen; Library is oilor site i: Not!; Site 2: EcoNV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen; and 20-22 week male spleen; Library is oiloodT primed and directionally cloned (EcoNV site is destroyed upon cloning). Average insert size 1.4 kb, insert size upon cloning is normalized and enriched for range 1.3 kb, Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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SINH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMNIST) row: a column: 12
High quality sequence stop: 710.
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48.8%; Score 703; DB 4; Lk
Best Local Similarity 100.0%; Pred. No. 1.6e-176;
Matches 703; Conservative 0; Mismatches 0;
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BI767614.
BI767614.1 GI:15759192
EST.
Homo sapiens (human)
Homo sapiens (human)
BONALYOCA; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                            TGTAATATTAGGTCCACCCGCCTCAGGGAAAACAACAATAGCAATGTGGCCTCTGCAAACA 239
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                                                                                               CACCGAAGCCAGAAGGCTTTATCTGCAAAGGAAGACAGTTCCCAGCGCGCTGCTCCA
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                                       Gaps
                                     7;
   Length 827;
                                         Indels
     50.2%; Score 723.2; DB 4; 98.8%; Pred. No. 6.7e-182; iive 0; Mismatches 3;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 657)
Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dicot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingemith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
Vandenhatte,J., Cusick,M.B., Albala,J.S., Hill,D.B. and Vidal,M.
Human ORPeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
Genome Res. (2004) In press
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5180
Fax: 617 632 539
Email: Marc Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a POR reaction using an MGC full-length cDNA as
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657 bp mRNA linear EST 20-AUG-2004 sapient controlled to mRNA linear EST 20-AUG-2004 sapiens cDNA 5' similar to BC034776, mRNA sequence. CV030269 CV030269. GI:51488510 EST.
                                                                                                 ATCTTAAATGAGTTTTCCTATACGGCCACCGAAGCCAGAAGGCTTTATCTGCAAAGGAAG 333
                                                                                                                                                                                       334 ACAGTICCCAGCGCGCTCGTCCAGCTCATTCAGGAACGCCTGGCTGAAGAGGATTGC 393
                                                                                                                                                                                                                    ACAGTICCCAGCGCGCTCCTCCTGCTGATTCAGGAACGCCTGGCTGAAGAGATTGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                   634 GAGCTGGACACGCTCACAAACTGCTGGAGTATCATAGGAACATCGTCAGGGTCATTCCC 693
                                            AGAGACAACGACAATGTGCCCCAGGATTGTAATATTAGGTCCACCCGGCTCAGGGAAAACA
                                                                           ACATAGCATGTGGCTCTGCAACATCTGAACGGCAGTCTCCTCACCCTGGAGAACCTG
                                                                                                                                                                                                                                                                                                                                                         394 ATCAAGCAGGGCTGGATTCTGGATGGCATCCCTGAGACGCGTGAGCAGGCTCTGAGGATC
                                                                                                                                                                                                                                                                   361 ATCAAGCAGGCTGGATTCTGGATGGCATCCCTGAGAGGCGTGAGCAGGCTCTGAGGATC
                                                                                                                                                                                                                                                                                                    454 CAGACCCTGGGGATCACCCCAGACGTCATTGTGCTGAGTGCTCCAGACACGGTCCTG
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661 TCCTACCCCA 670
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Olone="IMMGE:5170137"
// Lissue_type="medulla"
// Library is normalized and enriched for full-length clones and was constructed by C. Gruber
// Linvitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                                                                                                                                           BIB28586 670 bp mRNA linear EST 04-OCT-2001
GICATIGIGCIGAGIGCICCAGACACGGICCIGAICGAGAAAACIIGGGGAAGAAIC 547
                                                             607
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                          GACCCTCAAACTGGAGAGATTTATCACACCACTTTGACTGGCCACCCGAATCTGAAATC
                                             601 CAGAACCGTCTCATGGTGCCAGAGACATCTCAGAGCTGGAGACGGCTCAGAAACTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 CCCGAGATGCCCCCAGTACGGGGGGGGGGACACCATCTTCGAGTTGATGCAGAACATGCTG
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al Similarity 100.0%; Pred. No. 1.1e-167;
670; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                             mRNA sequence.
BI828586
BI828586.1 GI:15940136
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                                                                                                                                                                                                                            /note="Vector: mixed; The ORFs were PCR amplified from the MGC (Nammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Nammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Pull-Length Human and Mouse CDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
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                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                         /tissue type="mixed"
/clone Tib="Full Length cDNA from the Mammalian Gene
Collection"
                                                                                                                                                                                                                                                                                                                                                              Score 656; DB 7; Length 657;
Pred. No. 5.8e-164;
0; Mismatches 1; Indel8
                                     Plate: 11055... row: 11 column: E
Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
High quality sequence start: 97
High quality sequence stop: 656
                             Std Error: 60.00
                                                                                                                                   1. .657
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
FORWARD: ATGGACGCCACTATCGCC
BACKWARD: CAGGGGATTTTCTTGGGCAGG
                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.8%;
Matches 656; Conservative
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| Jorganism="Homo sapiens" | Jorganism="Homo sapiens" | Jorganism="Homo sapiens" | Jorganism="mRNA" | Jorganism="mRNA" | Jorn="Estable | Jorganism="List | Jorganism 968 AGGAGATGGCAGTTCCTGACGCCTCCTCATGAAGGTGCTGAGCCAGCGCGTGGACCAGC 1028 AGGACTGCATCCAGAAAGGCTGGGTGCTACACGGCGTCCCGCGGGACCTCGACCAGGCAC 1087 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seg primer: M13 FORWARD 540 ö 62 900 907 9 BUG17945 UI-H-DFO-beu-d-15-0-UI.81 NCI_CGAP_DFO Homo sapiens CDNA clone UI-H-DFO-beu-d-15-0-UI 3', mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 721)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), 908 realagagereregeagagareaaccacerrregegaagerecagecerrerrana 848 recadececercrisecensanaracasecristenarscrisers Gaps ö Score 591, DB 5, Length 721; Pred. No. 1.4e-146; 0, Mismatches 2; Indels TAG_LIB=UI-H-DF0 TAG_SEQ=GTTAAGCGTC" Location/Qualifiers 1. .721 BU617945.1 GI:23284160 similarity 99.7%; Homo sapiens (human) Conservative

to an EcoR I adaptor, digested with Not I, and cloned directionally into pT/T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this Ibrary IsSURE-Lug metatastic chondrosarcoma TAG_IIB=UI-H-DTI metatastic chondrosarcoma TAG_EGE=AACTGTTCGG.	Ouery Match Best Local Similarity 99.6%; Pred. No. 8.3e-135; Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Qy 892 TGCTGTGGGCAACTGCTGAAAGGGCTGTGGCAGATAGGACCACGTTTGGCGAGCTCATC Db 675 TGCTGTGGGCAACTGCTGAAAGGGCTGTGAAAAGGACAACTGTGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAA	QY         952 CAGCCCTTCTTTGAAAAGAGATTCCTGACAGCTCCTCATGAAGTGCTGAGC         1011           Db         615 CAGCCCTTCTTTGAAAAGAGAGTTCCTGACAGCTCCTCTGAGAGTGCTGAGC         556           QY         1012 CAGCGCTGGACAGCAGCAGCATCCTGAGAGGTGCTCAGGGGTGCTCAGGGGTGCTCAGGGGTGCTCGGGGGTGCTCAGGGGTGCTCGGGGGTGCTCGGGGGTGCTCAGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCGGGGGTGCTCCGGGGGTGCTCCGGGGGTGCTCCGGGGGTGCTCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCGGGGTGCTCCCCGGGGTGCTCCCGGGGTGCTCCCCGGGGTGCTCCCCGGGGTGCTCCCCGGGTGCTCCCCGGGTGCTCCCCGGGTGCCCCCGGGGTGCTCCCCGGGTGCTCCCCCGGGTGCTCCCCCGGGTGCTCCCCCC	
	OY         1208 ACCTCHGTACAAGCCACCTCCCACCATGAGATCCAGCTCGCCTCTGCAGAACCCAA 1267           Db         359 ACCTCATGATACACCCTCCCACCATGAGATCCCCTCCTCCTGCAGAACCCAA 300           QY         1268 AGGATGCTGAAGAGCAGTCAAGCTGAAAATGGACCTGTTCTACAGGAACTCAGCTGAT 1327           Db         299 AGGATGCTGAAGAGCAGGTCAAGCTGAAAATGGACCTGTTCTACAGGAACTCAGCTGACT 1327           Db         299 AGGATGCTGAAGAGCAGGTCAAGCTGAAAATGGACCTGTTCTACAGGAACTCAGCTGACT 240	QY         1328 TGGAGCAGTTGTATGGGCGATCACCCTCAATGGGACCCAGACCCATACACAGTCT 1387           Db         239 TGGAGCAGTTGTATGGGTCGGCCATCACCCTCAATGGGGACCCATACACAGTCT 180           QY         1388 TCGAATACATCGAGAGTGGGATCATTAATCCCCTGCCCAACAAAATCCCCTGA 1440           Db         179 TCGAATACATCGAGAGTGGGATCATTAATCCCCTGCCCAACAAAATCCCCTGA 127	RESULT 12  BO016312  BO01631  BO016312  BO01631  BO016312  BO01631  B

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BP368808 Sugano cDNA library, testis Homo sapiens cDNA clone TST00249, mRNA sequence.
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                                                        Score 518.4; DB 6;
Pred. No. 4.2e-127;
0; Mismatches 196;
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Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, R.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godiki, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis E.D., Kanai, A., Kuvochkin, I.W., Lee, Y., Lenhard, B., L., Nongasya, A., Kuvochkin, I.W., Lee, Y., Lenhard, B., L., Magashima, T., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Petrovsky, N., Pillai, R., Poutius, Jul, Qi, D., Ramachandran, S., Petrovsky, N., Pillai, R., Poutius, Jul, Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringaald, M., Sandelin, A., Schneider, C., Semple, C.A., Sctoul, M., Shimada, K., Shneider, C., Semple, C.A., Sctoul, M., Shimada, K., Verzdo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Varay, Z., Zavolan, M., Zhu, Y., Zimmer, A., Yang, I., Miyazasi, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazasi, A., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazasi, A., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Rogers, J., Birrey, B. and Hayashizaki, Y., Sasaki, D., Shibata, K., Raya, J., Mirney, B. and Hayashizaki, Y., Rasaki, D., Shibata, K., Raya, J., Mirney, B. and Hayashizaki, Y., Rucka, J., Saka,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analygis of Full-Length Mouse CDNAs Compared with Runal Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence analysis (RISA) system--384-format computer-based methods for the mouse full-length CDNA computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a norredundant CDNA library. Genome Res. 11 (2), 281-289 (2001)

norredundant CDNA library. Genome Res. 11 (2), 281-289 (2001)

norredundant Sciences Center and Sequenced in Mouse Genome Genomic Sciences Center and Genome Science Laboratory in Riken Convention of Experimental Animal Research in Riken contributed to process to the second of the property of the second of the property of the second of the se
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9226
Fax: 81-45-503-9226
Fax: 81-45-503-9216
Famil: genome-reseggscriken.jp, URL:http://genome.gscriken.jp/
Adachi.J., Alzawa,K., Akhmra,T., Arakawa,T., Carninci.P.,
Adachi.J., Hashizume,W., Hayashida,K., Hirozame,T., Holi.F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Numazaki,R., Myazaki,A., Murata,M., Nakamura,M.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission.
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/clone="1190002A17"
/tissue type="whole body"
/dev stage="18-day embryo"
/clone lib="RIKEN full-length enriched, 18-day embryo
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/mol type="mRNA"
/strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 583)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
16-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yeuzuki@ims.u-cokyo.ac.jp.
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                                                                                                                                                                                            / Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Mob zref="taxon:9606"
/ Clone="SZB06383"
/ Lissue type="brain"
/ Clone_lib="Sugano CDNA library, brain"
                                                                                                                                                                                                                                                                                                       ch 35.7%; Score 513.8; DB 5; Il Similarity 98.9%; Pred. No. 6e-126; 548; Conservative 0; Mismatches 3;
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The invention relates to novel human polypeptides (NHP) having kinase

Claim 1; Page 38; 40pp; English.

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ALIGNMENTS

New human kinase proteins and polynucleotides, useful for cosmetic and nutriceutical applications, drug screening, clinical trial monitoring, diagnosing or treating diseases associated with biological disorders or imbalances. NHP; kinase; gene therapy; drug screening; human; gene; ds. NOvel human kinase polypeptide (NHP) encoding DNA. Location/Qualifiers
1. .1440
/*tag
/product= "NHP"
/note= "kinase polypeptide" Yu X, Xie Q, Abuin A, Walke DW; ABV75301 standard, DNA, 1440 BP. (LEXI-) LEXICON GENETICS INC. 08-MAY-2002; 2002WO-US014669. 09-MAY-2001; 2001US-0289727P. 07-MAR-2003 (first entry) WPI; 2003-103514/09. P-PSDB; ABB82701. WO200290517-A2 Homo sapiens. 14-NOV-2002. ABV75301; 

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activity and polynucleotides encoding them. The polynucleotides, proteins, antibodies, agonists and attagonists of the proteins are useful for drug screening, clinical trial monitoring, and diagnosing or treating faiseases or disorders associated with biological disorders or imbalances. The proteins and polynucleotides are useful in cosmetic and mutriceutical applications, for identifying protein coding sequences and mapping a multique gene to a particular chromosome. The sequence of the polynucleotides and proteins can also be used as additional DNA markers for restriction fragment length polymorphism analysis, or in forensic biology. The present sequence represents a NHP kinase encoding DNA
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841 MANACTCCAGACCCCCCTCCTGGCCCGAAATRAGAATTCTCTGTTTTTTTTTT	CTGTGGG 900	GCCCTTC 960	ACCCCTG 1020          ACCCCTG 1020	ACCTCGAC 1080          ACCTCGAC 1080	GAATGTG 1140           GAATGTG 1140	CTGGGGAA 1200          CTGGGGAA 1200	rcrgcag 1260          rccrgcag 1260	13	ACCCATAC 138	7 7	TCCCCIGA 144 TCCCCTGA 144					Nootropic; ancer; ne; ss.							nii S; Tamechika I	
841 P 841 P 841 P 901 C	GGCCGCCCTCCTGGCCCAGAAATACAGGCTTGTCAATGTCTGCT 	agaggtgtgggggaggggggtggggggggggggggggg	GATGGCAGTTCCTGACACCTCCTCATGAAGGTGCTGAGCCAG( 	CTGCATCCAGAAAGGCTGGTGCTACACGGGGGTCCCGGGGGGC 	GCTGAACGGCTGGGCTACAATCCCAACAGGGTGTTTTTCCTG 	catcatgagcgctgactctgagaagaattgatcggtcact 	CATGTACAAGCTCCCACCATGGAGATCCAGGTCGGCTCGCTC	TOTALGA MAGAGA CARANGA MAGA CATALACA CA MAGA MAGA CATALACA CA MAGA MAGA MAGA CATALACA CATALAC	AGCAGTTGTATGGGTCGGCCATCACCTCAATGGGGAACAGGACA	AGCAGTTGTATGGGTCGGCCATCACCCTCAATGGGGACCAGGAC	artacaticagacticggaricattartccccticcccaagaaati 	1579 BP		entry)	ce, SEQ ID 1381.					-0000658	-00328381 -0350435P	NST. SIOTECHNOLOGY.	Otsuki T, Wakamatsu A, Sato H, Ishi Hio Y, Otsuka K, Nagai K, Irie R, T Otsuka M, Nagahari K, Masuho Y;	
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                                          AAAAGTCTGCAGGCCGCCCTCCTGGCCCAGAATACAGGCTTGTCAATGTCTGCTGTGTGGG
                                                       Human; kinase and phosphatase; KPP; enzyme; cardiovascular disorder;
neurological disorder; cancer; gene therapy; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human kinases and phosphatases (KPP)-3 cDNA.
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/product= "KPP protein"
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15-JUN-2001; 2001US-0298712P.
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                         New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
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                                                                              The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                            0,
                                                                                                                                                       Query Match 100.0%; Score 1440; DB 10; Length 1579; Best Local Similarity 100.0%; Pred. No. 0; Matches 1440; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                    Sequence 1579 BP; 403 A; 467 C; 406 G; 303 T; 0 U; 0 Other;
                                                            Claim 1; SEQ ID NO 1381; 205pp; English
WPI; 2003-395539/38.
P-PSDB; ADA55452.
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                                                                                                                                                                                                                                                                                                 The invention relates to novel human kinases and phosphatases (KPP) polypeptides and polynucleotides. Polypeptides of the invention are used for screening agonists and antagonists. They are used to make monoclonal or polyclonal or antibodies, which are used in diagnostic tests for conditions or diseases associated with expression of the polypeptide. They are also useful for diagnosting or treating diseases or conditions associated with decreased expression or overexpression of functional KPP e.g. cardiovascular or neurological disorders or cancer. The invention is useful in gene therapy. The present sequence is human KPP cDNA
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                                                                                                                                                                                                                     New human kinases and phosphatases (KPP), useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional KPP e.g.,
                                                                                                             Yue H, Lu DAM, Azimzai Y, Ding L, Lee EA, Hafalia AJA, Becha SD; Tang YT, Lal PG, Griffin JA, Gururajan R, Ramkumar J, Elliott VS; Arvizu CS, Luo W, Swarnakar A, Duggan BM, Tran UK, Walia NK; Gandhi AR, Yao MG, Khan FA, Baughn MR, Borowsky ML, Zebarjadian Y; Richardson TW, Marquis JP, Chien D, Jin P;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1581 BP; 413 A; 464 C; 402 G; 302 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                  Claim 5; Col 154; 82pp; English.
            06-JUL-2001; 2001US-0303418P.
19-JUL-2001; 2001US-0308183P.
27-JUL-2001; 2001US-0308183P.
19-DEC-2001; 2001US-0343007P.
15-FEB-2002; 2002US-0357675P.
30-APR-2002; 2002US-0376988P.
                                                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                        2003-120774/11.
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P-PSDB; AAE34860.
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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in endocrine, con a creaning assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to the coding sequence for one of the polypeptides of the invention.
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                                                                                                                                                                                                                          Sequence 1623 BP; 409 A; 482 C; 419 G; 313 T; 0 U; 0 Other;
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Dipipo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo K, Herrmann DL, Hjalt T, Ji W, Kekuda R
Khramtsov NV, Li Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
Burgess CE, Lepley DM;
                                ds; gene; cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thyromimetic; NoVX; pathology; cancer; diabetes; obssity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.
Human NOVX polypeptide coding sequence SEQ ID NO: 129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; SEQ ID NO 129; 772pp; English.
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06-JUN-2001; 2001US-0295641P.
06-JUN-2001; 2001US-0296404P.
06-JUN-2001; 2001US-029641BP.
07-JUN-2001; 2001US-0296475P.
11-JUN-2001; 2001US-029575FP.
12-JUN-2001; 2001US-029573P.
12-JUN-2001; 2001US-0299582BP.
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19-JUN-2001; 2001US-0299582BP.
22-JUN-2001; 2001US-0299582BP.
23-JUN-2001; 2001US-0299583P.
24-JUN-2001; 2001US-0299948P.
25-JUN-2001; 2001US-039984P.
26-JUN-2001; 2001US-0301S90P.
28-JUN-2001; 2001US-0301S90P.
28-JUN-2001; 2001US-0301S90P.
28-JUN-2001; 2001US-0301S90P.
28-JUN-2001; 2001US-0301S90P.
21-PEB-2001; 2001US-031889PP.
22-PEB-2002; 2002US-035931P.
22-PEB-2002; 2002US-035931P.
22-PEB-2002; 2002US-035931P.
22-PEB-2002; 2002US-035931P.
22-PEB-2002; 2002US-035931P.
27-PEB-2002; 2002US-035931P.
27-PEB-2002; 2002US-035931P.
27-PEB-2002; 2002US-035931P.
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27-PEB-2002; 2002US-035931P.
27-PEB-2002; 2002US-0359344P.
10-MAR-2002; 2002US-0359344P.
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P-PSDB; ADC10110.
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84

9 97

Gaps

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337

324 397 444 517 504 577 564 637 624 697 684 757 744 817 804 877

Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Otsuka M, Nagahari K, Masuho Y;

HELIX RES INST. RES ASSOC BIOTECHNOLOGY.

T, Sugiyama T, to J, Isono Y, F

Yamamoto J,

Seki N,

Isogai T, (HELI-) | (REAS-) |

WPI; 2003-450961/43. P-PSDB; ADB65473.

05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978.

New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or

as targets of gene therapy.

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                                                                                            985 GACAGCCTCCTCATGAAGGTGCTGAGCCAGGGCCTGGACCAGGACTGCATCCAGAAA 1044
                                                                                                                       GECTGGGTGCTACACGGCGTCCCGCGGGACCTCGACCAGGCACACCTGCTGAACGGCTG 1104
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                GATAGGACCACGTTTGGCGAGCTCATCCAGCCCTTCTTGAAAAGGAGATGGCAGTTCCT
                                     GCCCAGAAATACAGGCTTGTCAATGTCTGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                        Human; 88; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
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/product= "Clone TEST120244460 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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28-MAR-2002; 2002EP-00007401

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The invention discloses a polymucleotide comprising a sequence selected from 1970 fully defined nuclectide sequences which encode novel control of the polymucleotide, an antibody binding to the polympetide or peptide or its partial peptide, an antibody binding to the polympetide or peptide of the polymucleotide, immunologically assaying the polympetide or peptide of the polymucleotide by contacting the polympetide or peptide or peptide of the polymucleotide by contacting the polympetide or peptide or between the two, a transformant carrying the polymucleotide in an observing the binding or between the two, a transformant carrying the polymucleotide in an or contact a primer for synthesising the polymucleotide in an order of a useful as a primer for synthesising the polymucleotide or as a probe or contact and an antisense polymucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related contactions for regulation of their expression and activity, or as targets of gene may be included in them, for developing a diagnostic marker or configurate proteins, signal transduction-related proteins, capanal transduction-related proteins, signal transduction-related proteins, capanal transduction-related proteins, capanal diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded proteins of the sequence conting them can be used as indicacors for diseases. The charaction by a capanal capanal diseases (e.g. osteoporosis, encoding them can be used as indicacons for diseases. The charaction of the invention. Note: Some of the sequence of the activity or expression of the invention of the code of the encoded proteins of the sequence of the activity 
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Claim 1; Page; 222pp; English
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1772; Conservative
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de; gene; cytostatic; antidiabetic; anorectic; cerebroprotective; burucprotective; antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX; pathology; cancer; diabetes; obssity; endocrine disorder; CS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.
                                       Human NOVX polypeptide coding sequence SEQ ID NO: 127.
                                                                                                                                                                    04-JUN-2001; 2001US-0295601P.
06-JUN-2001; 2001US-029561P.
06-JUN-2001; 2001US-029561P.
06-JUN-2001; 2001US-029561P.
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14-JUN-2001; 2001US-029852P.
15-JUN-2001; 2001US-029938P.
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15-JUN-2001; 2001US-029938P.
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23-JUN-2001; 2001US-029939P.
23-JUN-2001; 2001US-03993P.
24-JUN-2001; 2001US-03993P.
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25-JUN-2001; 2001US-03993P.
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28-JUN-2001; 2001US-0301S9P.
28-JUN-2001; 2001US-0301S9P.
28-JUN-2001; 2001US-0318458P.
21-FEB-2002; 2002US-035897RP.
22-FEB-2002; 2002US-0359934P.
23-FEB-2002; 2002US-0359934P.
24-FEB-2002; 2002US-0359944P.
25-FEB-2002; 2002US-0359944P.
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                                                                                                        Homo sapiens.
                       18-DEC-2003
CTGTGGCAGATAGGACCACGTTTGGCGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGG 976
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Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E, Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA, Getlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R, Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I, Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK, Schenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK, Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP, Burgess CE, Lepley DM, (CURA-) CURAGEN CORP.

WPI; 2003-210149/20. P-PSDB; ADC10108.

New isolated NOVX polypeptides and nucleic acid molecules useful for

ADC10107 standard; DNA; 1967 RESULT 6 ADC10107 ID ADC

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                                                                                                     The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to the coding sequence for one of the polypeptides of the invention.
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treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.
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Best Local Similarity 90.8%; Pred. No. 1.7e-293;
Matches 1308; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                        New adenylate kinase polypeptide for diagnosing/treating cellular
proliferative and/or differentiative, neurological, immune, inflammatory,
lymphatic, cardiovascular, respiratory and hematological disorders.
119. .992
/*tag= b
/note= "This region is specifically referred in claim 2"
219. .386
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                                                                                                 387. .992
/*tag= c
/product= "Human mature 27802 adenylate kinase"
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                                                                                                                                                                                                                                                                                                    Kapeller-Libermann R,
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P-PSDB; AAE07843.
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GCTGACTTGGAGGAGTTGTATGGGTCGGCCATCACCCTCAATGGGGACCAGGACCCATAC 1380
                     /*tag= a /product= "Human 27802, adenylate kinase protein" /product= "Human 27802, adenylate kinase protein" 219. 774 /*tag= b /note= "This region is specifically claimed as SEQ ID NO: 23 in claim 1 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel proteins including ATPase-like proteins, phosphatidylserine synthase-like proteins, DNA fragmentation factor-like proteins or adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polypeptides including phosphatidylserine synthase-like polypeptide useful for identifying a compound which binds and modulates activity of the polypeptide useful for treating diseases, e.g. cancer.
                                                                                                                                                                                                                                                                           Human; ATPase-like protein; phosphatidylserine synthase-like protein; DNA fragmentation factor-like protein; vesicle-mediated transport; phospholipid scramblase-like protein; adenylate kinase protein; organelle biogenesis; cell-cycle regulation; primary brain lymphoma; protein degradation; splenomegaly; pulmonary embolism; Hodgkin disease; atresta; tuberculosis; astrocyte; apoptosis; neurodegenerative disease; DNA fragmentation; autoimmune disorder; cancer; blood clotting system; immune system; haematopoietic; hypertension; systemic sclerosis; atherosclerosis; leukopaenia; oligodendrocyte; gene; ss.
                                                          1381 ACACTCTTCGAATACATCGAGAGTGGGATCATTAATCCCCTGCCCAAGAAATCCCCTGA
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                                                                                                                                                                                                                                                      adenylate kinase cDNA.
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12-FEB-2001; 2001US-00781577.
21-FEB-2001; 2001US-00790179.
21-FEB-2001; 2001US-00790180.
22-FEB-2001; 2001US-00790838.
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2000US-0185946P.
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29-FEB-2000;
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cc kinase proteins and polynucleotides encoding such proteins. The human ATPase-like molecules are useful for modulating ATPase function. They are useful in modulating organelle biogenesis, cell-cycle regulation, protein degradation and vesicle-mediated transport. They are also useful for treating disorders associated with aberrant ATPase-like expression or activity such as splenomegaly, pulmonary embolism, atrests and primary cc activity such as splenomegaly, pulmonary embolism, atrests and primary cc useful for modulating the biosynthetic pathway involving the synthesis of the membrane phosphatidylserine (FS). They human phosphatidylserine cysprubase-like molecules are useful for treating disorders associated with aberrant human phosphatidylserine (FS). They human phosphatidylserine (FS). They human phosphatidylserine (FS) astrocytes and Hodgkin disease. The human 5698, DNA fragmentation factoristem are useful for modulating apportor events, including DNA fragmentation. The human 5698 molecules are useful for treating diseases cut as autoimmune, haematopoietic and blood clotting systems. They are modulating immune, haematopoietic and blood clotting systems. They are useful for treating a disorders associated with aberrant human cuseful for treating a disorder associated with aberrant human cyspendiating cellular growth and/or cellular metabolic pathways. They are cuseful for treating hypertension, atherosclerosis and oligodendrocytes. The present sequence is human 27802, adenylate kinase conn
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71.7%; Score 1032.8; DB 10; Length 1452;
Best Local Similarity 86.5%; Pred. No. 8.3e-259;
Matches 1246; Conservative 0; Mismatches 2; Indels 192; Gaps
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4-FEB-2000; 2000US-013664F.
20-MAR-2000; 2000US-013664F.
10-MAR-2000; 2000US-0136026P.
11-MAR-2000; 2000US-0139027P.
11-MAR-2000; 2000US-0139027P.
13-MAY-2000; 2000US-0139123P.
13-MAY-2000; 2000US-0139123P.
13-MAY-2000; 2000US-0139123P.
13-MAY-2000; 2000US-0139123P.
11-JUL-2000; 2000US-021488FP.
11-JUL-2000; 2000US-021488FP.
11-JUL-2000; 2000US-021488FP.
11-JUL-2000; 2000US-021488PP.
11-JUL-2000; 2000US-021489P.
11-JUL-2000; 2000US-021629P.
14-JUL-2000; 2000US-021629P.
14-JUL-2000; 2000US-022164PP.
14-JUL-2000; 2000US-022164PP.
14-JUL-2000; 2000US-022526FP.
14-JUL-2000; 2000US-022575FP.
14-JUL-2000; 2000US-02257FP.
14-SEP-2000; 2000US-02237FP.
14-SEP-2000; 2000US-02337FP.
14-SEP-2000; 2000US-02337FP.
14-SEP-2000; 2000US-02337FP.
14-SEP-2000; 200US-02337FP.
14-SEP-2000; 2000US-02337FP.
14-SEP-2000; 200US-02337
                                                                                                                      17-JAN-2001; 2001WO-US001312
 acquired immune
                                                            WO200154733-A1
                                 Homo sapiens.
TITGAAAAGGAGATGGCAGITCCTGACAGCCTCCTCATGAAGGTGCTGAGGCCAGCGCCTG 1020
                                                                                                                                                                                                                                                                                                                                                                        1021 GACCAGCAGGACTGCATCCAGAAAGGCTGGTGCTACACGGCGTCCCGCGGGACCTCGAC 1080
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                                                                                                                                                                                                                                                                   Neuroprotective, cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; cancer; immune system disorder; rheunatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; rheunacogenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; ss;
   AGTGCTGACCAGCCATGTGTGGACGTCTTCTACCAGGTCTGACCTATGTCCAAAGCAAC
                                                                                                                           CATCGTACTAATGCCCCGTTCACCCCGAGGGTGCTGCTGCTGGGCCCTGTGGGGAGTGGG
                                                                                                                                                                                      cDNA encoding novel signal transduction pathway protein, Seq ID 257.
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AAS2722
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000US-0246609P
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08-NOV-2000; 20
08-NOV-2000; 20
08-NOV-2000; 20
20-OCT-2000;
01-NOV-2000;
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Ruben SM (HUMA-) HUMAN GENOME SCI INC 

Rosen CA, Barash SC,

WPI; 2001-465460/50. P-PSDB; AAU17305.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

Claim 1; SEQ ID NO 257; 880pp; English.

The invention relates to novel isolated polypeptides (I), and polymucleotides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune configurates (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rhematoid arbitrits), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (c.g. disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. disorders, primary haematopoietic disorders, primary haematopoietic disorders, chromosomal abnormalities (c.g. daucher, s disease, Parkinson's disease), chromosomal disorders (e.g. alzheimer's disease), reprovative disorders (e.g. stroke), renal disorders (e.g. confinentions), crespiratory disorders, dermatological disorders (e.g. arrhythmia), crespiratory disorders, dermatological disorders (e.g. Addison's cinflammatory disorders), liver disorders, gastrointestinal disorders (inflammatory disorders) liver disorders (cirrhosis), as stimulators of cinflammatory disorders), liver disorders (cirrhosis), as stimulators of higher affinity antibodies, and as a means to induce tumour proliferation hathologies e.g. acquired immune deficiency syndrome (ADS). AAS20976-AAS27850 represent novel signal transduction pathway protein coding

Query Match 71.4%; Score 1027.6; DB 4; Length 1223; Best Local Similarity 95.6%; Pred. No. 1.8e-257; Matches 1153; Conservative 0; Mismatches 10; Indels 43; Gaps

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Parkinson's
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                                                                    31-JAN-2000; 2000US-0179065P.
28-UJN-2000; 2000US-0116647P.
07-UJU-2000; 2000US-0216647P.
07-UJU-2000; 2000US-0216647P.
11-UJU-2000; 2000US-0216680P.
11-UJU-2000; 2000US-0217496P.
11-UJU-2000; 2000US-0217496P.
11-UJU-2000; 2000US-022064P.
14-AJG-2000; 2000US-022064P.
14-AJG-2000; 2000US-0225267P.
14-AJG-2000; 2000US-0225347P.
14-AJG-2000; 2000US-0225347P.
14-AJG-2000; 2000US-0225347P.
14-AJG-2000; 2000US-0225347P.
15-SEP-2000; 2000US-0225347P.
15-SEP-2000; 2000US-0225347P.
25-SEP-2000; 2000US-0229342P.
25-SEP-2000; 2000US-0229342P.
25-SEP-2000; 2000US-0239343P.
25-SEP-2000; 2000US-0239342P.
25-SEP-2000; 2000US-0239342P.
25-SEP-2000; 2000US-023933P.
25-SEP-2000; 2000US-023933P.
25-SEP-2000; 2000US-023933P.
25-SEP-2000; 2000US-023939P.
26-CCT-2000; 2000US-023939P.
26-CCT-2000; 2000US-023939P.
26-CCT-2000; 2000US-023939P.
26-CCT-2000; 2000US-023939P.
27-SEP-2000; 200US-023939P.
27-SEP-2000; 200US-023939P.
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27-SEP-2000; 200US-023939P.
27-SEP-2000; 200US-023939P.
27-SEP-2000; 200US-023939
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P-PSDB; ADB94013.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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CCTGACAGCCTCCTCATGAAGGTGCTGAGCCCAGGCCTGGACCAGCAGGAGCTGCATCCAG 1041
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                                                             GAGGACATCTCAGAGCTGGAGACGGCTCAGAAACTGCTGGAGTATCATAGGAACATGGTC (
     GCTCTGAGGATCCAGACCCTGGGGATCACACCCAGACACGTCATTGTGCTGAGTGCTCCA
                      Human cDNA encoding a novel protein #247.
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pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the polypeptide. The polypeptide is also useful for identifying a binding partner and determining whether the binding partner and determining whether the binding partner ceffects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid pathological condition in a subject, which involves determining the presence or absence of a mutation in The nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility and suspective or absence of the mutation in the suspectibility or the polypeptide, the suscept sequence represents sequence represents sequence represents sequence represents sequence or susceptibility and su seqdata.uspto.gov/sequence.html?DocID=20020168711. \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Sequence 1223 BP; 305 A; 355 C; 310 G; 245 T; 0 U; 8 Other;

423 441 501 542 381 85 AACATGCTGGAGCAACTCCTGATCCACCAGCCCGAAGATCCCATCCCTTCATGATCCAG 144 145 CACTIGCATAGAGACAACGACAATGIGCCCAGGAITGIAATAITAGGICCACCGCCICA 204 263 303 321 1 ATGGACGCCACTATCGCCCCCGCACGTATCCCCCCGAGATGCCCCCAGTACGGGGAGGAG 60 61 AACCACATCTTCGAGTTGATG-----CAG 84 GGA-GAACCTGATCTTAAATGAGTTTTCCTATACGGCCACCGAAGCCAG-AAGGCTTTAT GAAGAATTGCATCAAGCAGGCTGGATTCTGGATGGCATCCTGAGACGCGTGAGCAG GCTCTGAGGATCCAGACCTGGGGATCACCCAGACACGTCATTGTGCTGAGTGCTCCA GACACGGTCCTGATCGAGAGAAACTTGGGGAAGAGAATCGACCCTCAAACTGGAGAGATT 244 GGGAAAACAATAGCAATGTGGCTCTGCAAACATCTGAAACAGCAGAGTCTCCTCACCCT CTGCAAAGGAAGACAGTTCCCAGCGCTGCTCGTCCAGCTGATTCAGGAACGCCTGGCT GGGAAAACAACAATAGCAATGTGGCTCTGCAACATCTG-AACAGCAGTCTCCTCACCCT Gaps DB 10; Length 1223; 43; 10; Indels 71.4%; Score 1027.6; DB 10 95.6%; Pred. No. 1.8e-257; ative 0; Mismatches 10; Query Match Best Local Similarity 95.6 Matches 1153; Conservative 304 322 364 382 424 442 483 502 205 264 요 요 8 유 ઠે 원 ò 요 셤 ઠે 셤 Š ð 셤 ð ò

රු සි	562 TAICACACCACCITIGACTGGCCACCCGATCTGAAATCCAGAACCGTCTCATGGTGCCA 621
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ð í	2 CTGGGCTACAA-TCCCAACAGGGTTTTTCCTGAATGTGCCATTTGATTCATTTGATTCATGGA 120
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RESULT AAD2647	LT 11 SAD26472 standard: CDNA; 995 BP.
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E X	26-MAR-2002 (first entry)
ă X	
<b>E E</b>	Human; kinase; PKIN-25; cancer; leukaemia; adenocarcinoma; osteoporos1s; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
K.	Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
X X	
X X	Good pasture's syndrome; Graves ulsease; panciouries; portries theumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; rheumatoid arthritis; ulcerative colitis; cirrhosis; cushing sectoris;
X X	neparitis; nypothytorusem, coronary project cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; cardiovascular disease; lung tumour; gout;
ž ž	Congretive meann-Pick's disease; gene therapy; ss.
¥8\$	Homo sapiens.
HELE	Key Location/Qualifiers CDS 43870 /*tag= a
FT	/product= "Human PKIN-25 protein"

482

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us-10-798-773-1.xng

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1053 GCTACACGGCGTCCCGCGGGACCTCGACCAGGCACACCTGCTGAACCGCCTGGGCTACAA 1112
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                                                                                                             GCTGCTCGCGCCCTCTGGGCAGTGGGAAAAGTCTGCAGGCCGCCCTCCTGCTGGCCCAGAA
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                        GCTGCTGCTCGGGCCTGTGGGAAAAGTCTGCAGGCCGCCCTCCTGGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.
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                                                                                                                                                                                                                                                                                                          Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y, Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT; Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Batra S, Ison CH;
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                                                                                                               15-JUN-2000; 2000US-0213673P.
23-JUN-2000; 2000US-021367P.
30-JUN-2000; 2000US-0216651P.
13-JUL-2000; 2000US-021660SP.
25-AUG-2000; 2000US-021837ZP.
                                                                           14-JUN-2001; 2001WO-US019444
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P-PSDB; AAE16279.
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                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                              CCCAAAATCCTCAAAGTCATCAGTGCTGACCAGCCATGTGTGGACGTCTTCTACCAGGCT
                                                                                                                                                                                                                                     CTCGGGCCTCTGTGGGAAAAGTCTGCAGGCCGCCCTCCTGGCCCAGAAATACAGG
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                                                                                                                                                                            CTGACCTATGTCCAAAGCAACCATCGTACTAATGCCCCGGTTCACCCCGAGGGTGCTGCTG
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2000US-00653450.
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2000US-00488725.
2000US-00552317.
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03-AUG-2000; 2
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29-NOV-2000;
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25-APR-2000;
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Yang Y,
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Pred. No. 7e-188;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                         vel nucleic acids and polypeptides, useful central nervous system injuries.
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irman T, Xu C, )
Drmanac RT;
                                     23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-0055317.
20-JUN-2000; 2000US-0055317.
19-JUL-2000; 2000US-0065312.
03-AUG-2000; 2000US-0065312.
03-AUG-2000; 2000US-0065312.
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Local Similarity 92.0%;
hes 803; Conservative (
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Wehrman T,
              26-DEC-2000; 2000WO-US034263
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Wang Z, Wehrn
Goodrich R, I
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P-PSDB; AAM38895.
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Wang J,
Zhou P,
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Zhao QA;
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                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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      Ren F, Wa
Zhang J,
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 721 BP; 178 A; 212 C; 188 G; 143 T; 0 U; 0 Other;
      Qian XB,
Yang Y,
   Liu C, Agundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RI;
                                                                                                                                         Claim 1; SEQ ID NO 3826; 10078pp; English.
                                                        WPI; 2001-442253/47.
P-PSDB; AAM40681.
Tang YT,
Wang J, V
Zhou P, G
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Human; dithp; diagnostic and therapeutic polynucleotide; gene; se; bone; cell proliferative disorder; cancer; tumour; autoimmune disorder; brain; inflammatory disorder; viral infection; bacterial infection; seizure; fungal infection; parasitic infections; developmental disorder; breast; endocrine disorder; metabolic disorder; ineurological disorder; cervix; gastrointestinal disorder; transport disorder; gene therapy; kidney; adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human diagnostic and therapeutic (dithp) polynucleotides and their associated polypeptides (DITHP polypeptides).
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CTCGGGCCTGTGGGCAGTG 838
                                                              721
                                                                                                                                                                                                                                        BP
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05-SEP-2000; 2000US-0229748P.
05-SEP-2000; 2000US-0229749P.
05-SEP-2000; 2000US-0229750P.
05-SEP-2000; 2000US-0229751P.
06-SEP-2000; 2000US-0230581P.
06-SEP-2000; 2000US-0230514P.
06-SEP-2000; 2000US-0230518P.
06-SEP-2000; 2000US-0230518P.
06-SEP-2000; 2000US-0230518P.
06-SEP-2000; 2000US-0230518P.
06-SEP-2000; 2000US-0230518P.
06-SEP-2000; 2000US-023059P.
07-SEP-2000; 2000US-023098P.
07-SEP-2000; 2000US-023098P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human dithp polynucleotide #3
                                          703 CTCGGGCCTGTGGGCAGTG
                                                                                                                                                                                                                                    ABK71537 standard; cDNA; 615
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P-PSDB; ABG59945.
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                                                                                                                                                                                                                                                                                                          ABK71537;
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vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.

Homo sapiens.

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TGTAATATTAGGTCCACCCCCCCCAGGGAAAACAACAATA-GCAATGTGGCTCTGCAAAC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences of the invention are used in the treatment and diagnosis of cell proliferative disorders (e.g. atherosclerosis, cirrhosis, cancers (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis), viral infections, bacterial infections, infections, developmental disorders (e.g. anaemia, epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), emdocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. unceral sclerosis, multiple sclerosis), gastrointestinal alisorders (e.g. unceralive colitis, lysinuria) and transport disorders (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences ABK71535-ABK71809 represent human dithp polynucleotides of the invention
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                                                                                                                                                                                                                                                                                                                 y Match 39.9%; Score 574; DB 6; I Local Similarity 99.7%; Pred. No. 2.8e-139; hes 596; Conservative 0; Mismatches 0;
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Cao Y; R, Wang ZW;

Xu C,

Asundi V, Zhou P, X J, Zhang J, Ren F, Goodrich R;

Drmanac RT, A Wang D, Wang J Wejhrman T, G

zhao QA, W Liu C,

Tang YT, Ma Y, Zha Xue AJ,

03-PEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875. 20-UTM-2000; 2000US-00598075. 19-UTL-2000; 2000US-0050325. 01-SEP-2000; 2000US-00653561.

05-FEB-2001; 2001WO-US004098

09-AUG-2001

20-OCT-2000; 2000US-00693325 30-NOV-2000; 2000US-00728422

(HYSE-) HYSEQ INC.

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1216 TACAAGCCACCACCACCACGAGATCCAGGCTCGCCTCCTGCAGAACCCAAAGGATGCT 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynuclectides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemacopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, archritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1036 ATCCAGAAAGGCTGGGTGCTACACGGCGTCCCGGGGACCTCGACCAGGCACACCTGCTG
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Best Local Similarity 99.8%; Pred. No. 2.4e-110;
Matches 464; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 714-715; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476283/51.
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Human polynucleotide SEQ ID NO 95.

(first entry)

06-NOV-2001

AAK51550

BP

AAK51550 standard; cDNA; 997

g	647	647 TACAAGCCACCTCCCACCATGGAGATCCAGGCTCGCTGCAGAACCCAAAGGATGCT 706	ıo
ò	1276	GAAGAGCAGGTCAAGCTGAAAATGGACCTGTTCTACAGGAACTCAGCTGACTTGGAGCAG	2
qa	707	707 GAAGAGCAGGTCAAAGCTGAAATGGACCTGTTCTACAGGAACTCAGCTGACTTGGAGCAG 766	
ò	1336	1336 TTGTATGGGTCGGCCATCACCCTCAATGGGGACCAGGACCCATACACAGTCTTCGAATAC 1395	5
୍ଦୁପ	767	767 TIGTATGGGTCGGCCATCACCTCAATGGGGACCCAGGACCCATACACAGTCTTCGAATAC 826	
ò	1396	ATCGAGAGTGGGATCATTAATCCCCTGCCCAAGAAAATCCCCTGA 1440	
QQ	827	827 ATCGAGAGTGGGATCATTAATCCCCTGCCCAAGAAATCCCCTGA 871	
Search Job tim	Search completed: Ma Job time : 787 secs	Search completed: March 19, 2005, 20:53:48 Job time : 787 secs	

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AC015488 Homo sapi AL161726 Homo sapi AC064719 Homo sapi AL161726 Homo sapi AL161726 Homo sapi AL13536 Rattus no AC11353 Rattus no AC113252 Rouse DNA AC073291 Mus muscu AC00392 Genomic s AL731851 Mouse DNA AC02847 Rattus no AC061852 Genomic sapi AC66688 Oryza sat AC06688 Oryza sat AC060898 Gallus ga AL334533 Leishmani AT135924 Trypanoso Continuation (4 of AC002096 Homo sapi AX133763 Arabidops

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61 AACCACATCTTCGAGTTGATGCAGAACATGCTGGAGCAACTCCTGATCCACCAGCCCGAA 120
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BD027242
BD027242
AX06.1825
AX06.6688
CR389850
LMFLG294
AY1.69824
LMFLCHR36_02
LMFLCHR36_02
AX002096
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Sequence 1 from patent US 6734010.
AR534560 1GI:53924889
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AC015488
AL161726
AC084719
AL161726
AL145645
AC135345
AC118353
AL732526
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Length 1440; Indels

Qy 1381 ACAGTCTTCGAATACATCGAGAGTGGGATCATTAATCCCTGCCCAAGAAATCCCTGA 1440 	RESULT 2 AX714697 LOCUS DEFINITION Sequence 1381 from Patent EP1293569. ACCESSION AX714697 AX714697 AX714697 AX714697 AX714697 AX714697.1 GI:29889650	ACETWORDS SOURCE Home sapiens (human) SOURCE Home sapiens ORGANISM Home sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE 1 AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and		FEATURES Location/Qualifiers  11579  Corgania="Homo sapiens" /mol tyme="uned DNA"	o_xref="taxon:9606"	DB 6; Length 1579; 0; Indels 0; Gaps	AGGAG 			181 GTAATATAGGTCCACCCGCCTCAGGAAAACAATAGGAATGTGGCTTGCAAACAT 	241 CTGAACAGCAGTCTCCTCACCCTGAAAACCTGATTTTTTTT	301 ACCGAAGCCAGAAGGCTTTATCTGCAAAGGAAGAAGAAGTTCCCAGGGGGGGG	361 CTGATTCAGGAACGCCTGGCTGAAGAGGATTGCATCAGGAGGCTGGATTCTGGATGGC	Qy 481 GTCATTGTGCTGGTGCTCCAGACAGTCCTGATCGAGAAAGAA
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14. GACCTCOAACTGGAGGATTTATCACACCACCTTTAGCTGGCACCCCCAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGCACAACTCCAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCCACAAACTCACACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAACTCACAAAAACTCACAAAAACTCACAAAAACTCACAAAAACTCACAAAAACTCACAAAAAA	REFERENCE AUTHORS	TITLE	JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	COMMENT COMMENT FEATURES GOURC
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	GACCCTCAAACTGGAGAGATTTATCACACCACCTTTGACTGGCCACCCGAATCTGAAATC  [	CATCGTACTAATGCCCCGTTCACCCCGAGGGTGCTGCTGCGGGCCTGTGGGGCAGGGGGCTCTCAATGCCCTGTGGGCAGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGGGGGCTGGTGG	GAGCAGCACCACCTGAAAGGCTGGGTGCTACACGGCGTCCCGCGGGGACCTCGACCGCGGGCACCTCGACCGCGGCACCTCGACCGCGCGCACCACGCGCGCACCACGCGCGCACCCGCGGGGCTCCCGCGGGGCTCCCGCGGGGCTCCTCGACCGCGCACCCGCGGGGCTCCTCGACCGCCTCGACCGCCTCGACCGCCTCGACCGCCTCGACCGCCTCGACCGCCTCGACCGCCTCGACCGCCTCGACCGCCTCGACCGCCTCGACACGGCTTTTTTCCTGAATGTCCCATTTTTTCCTGAATGTCCCATTTTTTCCTGAATGTCCCATTTTTTTT	1290 PACCCAAAGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTG

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radmmatla; butnetta; filmates; Catallini; Comminitae; Incommenta; Figure Catallini; Catalli; Catalli 1440 1349 1469 1020 1049 AGGTACCACCTCATGTACAAGCCACCTCCCACCATGGAGATCCAGGCTCGCCTCCTGCAG 1260 1 linear PRI 29-JUN-2004 frame 98, mRNA (cDNA clone 989 Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1170 ccartreatrccarcargeaeceecreacrercagaagaarrearcagreacregeaaa **AACCCAAAGGATGCTGAAGAGCAGGTCAAGCTGAAAATGGACCTGTTCTACAGGAACTCA** GCTGACTTGGAGCAGTTGTATGGGTCGGCCATCACCCTCAATGGGGACCAGGACCATAC 1050 GACCAGCAGGACTGCATCCAGAAAGGCTGCTGCTACACGGCGTCCCGCGGGACCTCGAC CAGGCACCCCTGCTGAACCGCCTGCGACTACAACCAGGGTGTTTTTCCTGAATGTG 930 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACCACGTTTGGCGAGCTCATCCAGCCCTTC TTTGAAAAGGAGATGCCAGTTCCTGACAGCCTCCTCATGAAGGTGCTGAGCCAGCGCCTG 990 TTTGAAAAGAGAGATGCCAGATTCCTGACAGCCTCCTCATGAAGGTGCTGAGCCAGCGCCTG GACCAGCAGGACTGCATCCAGAAAGGCTGGGTGCTACACGGCGTCCCGGGGGACCTCGAC Homo sapiens chromosome 9 open reading MGC:35281 IMAGE:5175757), complete cds. BC034776.1 GI:21961344

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               GATCCCATCCCTTCATGATCCAGCACTTGCATAGAGACAACGACAATGTGCCCAGGATT
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                                                                                                                                                                                                VIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: capbs=r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: 1 Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22749186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found
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                                                                      Strausberg, R.
Direct Submission
Submitted (24-UL-2002) National Institutes of Health, Mammalian
Submitted (24-UL-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/lab hoste="NH10B"
/note="Vector: pCMV-SPORT6"
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100.0%; Score 1440; DB 9; Length 1656;
Best Local Similarity 100.0%; Pred. No. 0;
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Proc. Natl. Acad. Sci. U.S.A. 99
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                                                     (bases 1 to 1656)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAACAGCAGTCTCCTCACCCTGGAGAACCTGATCTTAAATGAGTTTTCCTATACGGCC
Series: IRAK Plate: 107 Row: i Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAACAGCAGTCTCCTCACCTGGAGAACCTGATCTTAAATGAGTTTTCCTATACGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="chromosome 9 open reading frame 98"
/protein_id="AAB15056.1"
/bxref="G1:30046788"
/db_xref="LocusID:158067"
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                                                                                                                                                                                                                                                                                     /tissue type="Brain, adult medulla"
/clone Tib="NIH MGC_119"
/lab_host="DH10B"
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                                                                                                                                                                                                          /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1440;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="synonym: FLJ32704"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="LocusID:158067"
                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557. .1996
/gene="C9orf98"
                                                                                                                                                                                                                                                                                                                                                                                                                            gene="C9orf98"
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Best Local Similarity 100.0
Matches 1440; Conservative
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Klausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Alschul, S.F., Zeeberg, B., Buetow, K.H., Scheefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Heieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Boutfeard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., St., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Munan and mouse CDNA sequences
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Contact: MGC help desk
Bmail: cgapbe-rømail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 9 open reading frame 98, mRNA (cDNA clone RCS:57747 IMAGE:5744517), complete cds.
                AACCCAAAGGATGCTGAAGAGCAGGTCAAGCTGAAAATGGACCTGTTCTACAGGAACTCA 1320
                                                                                                                                      AACCCAAAGGATGCTGAAGAGGAGGTCAAGCTGAAAATGGACCTGTTCTACAGGAACTCA 1373
                                                                                                                                                                                                            GCTGACTTGGAGCAGTTGTATGGGTCGGCCATCACCCTCAATGGGGACCAGGACCCATAC 1380
                                                                                                                                                                                                                                              1374 GCTGACTTGGAGCAGTTGTATGGGCCCATCACCCTCAATGGGGACCAGGACCCATAC 1433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2185)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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VERSION
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REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  REFERENCE 1 AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Yloshikawa,T., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagai,K., and	Masuho, Y.  TITLE Full-length CDNA sequences JOURNAL Patent: EP 1308459-A 1657 07-MAY-2003; Helix Research Institute (JP) ; Research Association for	Biotechnology (JP)  FEATURES Location/Qualifiers  source 11619 /organism="Homo sapiens"	/mol_type="mRNA" /db_xref="taxon:9606" ORIGIN	Query Match 81.2%; Score 1170; DB 6; Length 1619; Best Local Similarity 93.3%; Pred. No. 2e-271; Matches 1272; Conservative 0; Mismatches 0; Indels 92; Gaps	OY 169 GTGCCCAGGATTGTAATATTAGGTCCACCGCCTCAGGGAAACAACAATAGCAATGTGG 228	Oy 229 CTCTGCAAACATCTGAACAGCAGTCTCCTCACCCTGGAGAACCTGATCTTAAATGAGTTT 288	QY 289 TCCTATACGGCACCGAAGGCTTTATCTGCAAAGGAAGACAGTTCCCAGGGG 348	OY 349 CTGCTCGTCCAGCTGATTCAGGAACGCCTGGCTGAAGAGATTGCATCAAGCAG 402	Qy 403 402  Db 388 GTTTCTTGTAATAGCGGCTTTCGAGTTTTCATCCGCTAATTCCAGTATCTGAGTTACGTG 447	Qy 403	508	497	Oy 557 AGATTTATCACCACCTTTGACTGGCCACCCGAATCTGAAATCCAGAACGTCTCATGG 616	Oy 617 TGCCAGAGGACATCTCAGAGACGGACTCAGAAACTGCTGGAGTATCATAGGAACA 676	Oy . 677 TCGTCAGGGTCATTCCCTCCTACCCCAAAATCCTCAAAGTCATGCTGACCAGCCAT 736	Qy 737 GTGTGGACGTCTTCTACCAGGCTCTGACCTATGTCCAAAGCAACGTCGTACTAATGCCC 796	Qy 797 CGTTCACCCCGAGGGTGCTGCTGCGGCCTGTGGGCAGTGGGAAAAGTCTGCAGGCCG 856
	QY     601     CAGAACCGTCTCATGGTGCCAGAGACATCTCAGAGCTGGAGACGGCTCAGAAACTGCTG     660       Db     1157     CAGAACCGTCTCATGGTGCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAACTGCTG     1216	QY 661 GAGTATCATAGGAACATCGTCAGGGTCATTCCCTCCTACCCCAAAATCCTCAAAGTCATC 720	QY       721 AGTGCTGACCAGCCATGTGTGGACGTCTTCTACCAGGCTCTGACCTATGTCCAAAGCAAC 780         Db       1277 AGTGCTGACCAGGCATGTGTGGACGTCTTCTACCAGGCTCTGACCTATGTCCAAAGCAAC 1336	QY         781 CATCGRACTANTGCCCCGTTCACCCCGAGGGTGCTGCTGCTGGGGCCTGTGGGCAGTGGG 840           Db         1337 CATCGTACTAATGCCCCGTTCACCCCGAGGGTGCTGCTGCGGGCCTGTGGGCAGGGG 1396	QY         841         AAAAGTCTGCGCCCTCCTGGCCCAGAAATACAGGCTTGTCAATGTCTGCTGTGGG         900           DD         1397         AAAAGTCTGCAGGCCCTCCTGGCCCAGAAATACAGGCTTGTCAATGTCTGCTGTGGG         1456	CAGCCCTTC	TTTGAAAAGGAGATGGCAGTTCCTGACACCTCCTCATGAAGGTGCTGAGCCAGCC	GACCAGCAGGACTGCATCCAGAAAGGCTGGTGCTACACGGCGTCCCGGCGGGACCTCCGAC 	Oy 1081 CAGGCACACCTGCTGAACCGCCTGGGCTACAATCCCAACAGGGTGTTTTTCCTGAATGTG 1140  Db 1637 CAGGCACACCTGCTGAACCGCCTGGGCTACAATCCCAACAGGGTGTTTTCCTGAATGTG 1696			Oy 1261 AACCCAAAGGATGCTGAAGAGCAGGTCAAAGTGGACCTGTTCTACAGGAACTCA 1320  Db 1817 AACCCAAAGGATGCTGAAGAGCAGGTCAAGCTGAAAATGGACCTGTTCTACAGGAACTCA 1876	Oy 1321 GCTGACTTGGAGCAGTTGTATGGGTCGGCCATCACCCTCAATGGGGACCAGGACCCATAC 1380	ATCCCCTGA		LOCUS AX748132 1619 bp mRNA linear PAT 20-JUN-2003 DEFINITION Sequence 1657 from Patent EP1308459. ACCESSION AX748132 CT.23132620	

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Nazusa-Kamatari, Kisarari, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDo human comba sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Hell:x Research Institute (HRI) (supported by Japan Key Technology Center etc.;; 5'- & 3'-end one pass sequencing: RAB, HRI, and Blotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Oozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Naguchi, S., Itoh, T., Shigeta, K., Senba, T., Mateumura, K., Oyama, M., Hata, H., Watanabe, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satch, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Wasuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fulimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T. Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., NBDO, human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 GTGCCCAGGATTGTAATATTAGGTCCACCCGCCTCAGGGAAACAACAACAACAATGGGATGTGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
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| Organism="Homo sapiens"
| Mrol_type="mRNA"
| Mb_xref="taxon:9606"
| Clone="TEST12024446"
| Cissue_type="testis"
| Cione_lib="TEST12"
| Clone_lib="TEST12"
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/db_xref="GI:21752321"
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Nat. Genet. 36 (1), 40-45 (2004)
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3 (bases 1 to 1619)
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Best Local Similarity 93.33
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                CCTCCTGGCCCAGAAATACAGGCTTGTCAATGTCTGCTGTGGGCAACTGCTGAAAGAGG
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oligo capping; fis (full insert sequence).
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127 134 133 146 139 146 63 63 10N N	SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human)  REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE AUTHORS AUTHORS TITLE TITLE TITLE TOTAL AI 16-AUG-2001; Millennium Pharmaceuticals, Inc. (US) Location/Qualifiers Location/Qualifiers Location/Qualifiers  1. 1452 COS COS ADA ATTALE AMANGE CRITICALINEFSYTATEARRIYLORRYLVESA LIVOTOS HIMMAND PROPEREDCINGGINELANDILERNILLENGILESHANDYLIER ADACREE "GI:15523816" LIVOTOS HIMMAND RESECTINGGILERNALINESSICTATERRIYLESHANDYLIER ANGRID REPORTERIYTHERILINGEPROPESET ORRIANDERPROPLIER ANGRID REPORTERIYLYLORRYLYLORYLORGER STRAINTURINGER SYTATEARRIYLIER ANGRED REPORTERIYLYLORGER SEED CHANDERPROPERE CORRIANDERPROPLIER ANGRED REPORTERIYLYLORGER SEED CHANDERPROPERE CORRIANDERPROPLIER APPLIANTED REPORTERIYLYLORGER SEED CHANDERPROPERE CORRIANDERPROPLIER APPLIANTISADOPCYDVEYQALTYRGELIQPFREKENAGCES"	Query Match         71.7%;         Score 1032.8;         DB 6;         Length 1452;           Best Local Similarity 86.5%;         Pred. No. 2.7e-238;         2.7e-238;           Matches 1246;         Conservative 0;         Mismatches 2;         1 ATGACGCCACTATCGCCCGACCGTACCCCCCAGACGGGGGGGG
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Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R.D., Colling, F. S., Wagner, L., Shenmen, C. M., Schuler, G.D.,
Klausner, R.D., Colling, F. S., Wagner, L., Shenmen, C. M., Schuler, G.D.,
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Intachenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavanit, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Moramson, R.D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Mazny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Sanchez, A., Whiting, M., Satteman, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Youchman, J. W., Green, E. D.,
Butterffeld, S., Krzywinski, M. I., Schiska, U., Shalka, U., Shalka, U., Sheill, D. E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
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Location/Qualifiers
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Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
CONA Library Arrayed by: School of Medicine, Stanford Caner,
Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) med@paxil.stanford.edu
Contact: (Dickson, Mark) med@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
BC079446
Rattus norvegicus similar to hypothetical protein FLJ32704, mRNA (cDNA clone MGC:94995 IMAGE:7115585), complete cds.
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butherla; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/db_xref="caxon:10116"
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/clone_lib="nuth MGC_237"
/lab_host="DH10B"
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Contact: MGC help desk
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Direct Submission
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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1. .1581
/ JGene="McC94995"
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Best Local Similarity 77.8%; Pred. No. 5.36-213;
Matches 1120; Conservative 0; Mismatches 320; Indels 0;
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tive 0; Mismatches 0;
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RESULT 11 AX211565

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PAT 06-SEP-2001
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                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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      linear
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Pred. No. 2.1e-172;
0; Mismatches 2;
                                                                                                                                                                                                                         27802, an adenylate kinase
Patent: WO 0159082-A 3 16-AUG-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Kapeller-Libermann, R. and Chun, M.
      AX211565 774 bp
Sequence 3 from Patent W00159082.
AX211565 AX211565.1 GI:15523817
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Best Local Similarity 99.7%;
Matches 761; Conservative (
                                                                                                       Homo sapiens (human)
Homo sapiens
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inncoln,S.E., Altus,C.M., Dufour,G.E., Chalup,M.S., Hillman,J.L.,
Jones,A., Yu,J.Y., Wright,R.J., Gietzen,D., Liu, Toomy,F., Yap,P.,
Jones,A., Yu,J.Y., Maright,R.J., Gietzen,D., Liu, Toomy,F., Yap,P.,
Boahl,C.R., Moniyama,M., Bradley,D., Rohagi,S., Harris,B.,
Roseberry,A.M., Gerstin,E.H., Peralta,C.H., David,M., Panzer,S.,
Flores,V., Daffo,A., Marwaha,R., Chen,A., Chang,S.C. and Inman,R.R.
Molecules for diagnostics and therapeutics
Patent: Wo 0220754-A 3 14-MAR-2002;
Incyte Genomics, Inc. (US)
                                                      PAT 07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AGATCCCATCCCCTTCATGATCCAGCACTTGCATAGAGACAACGACAATGTGCCCAGGAT 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 AGCTGATTCAGGAACGCCTGGCTGAAGAGGATTGCATCAAGCAGGGCTGGATTCTGGATG 418
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type==mRNA"
/db_xref==tacn:9606"
/noTe==Incyte ID No: LG:017108.4:2000SEP08"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.9%; Score 574; DB 6; Length 61: Best Local Similarity 99.7%; Pred. No. 1.5e-127; Matches 596; Conservative 0; Mismatches 0; Indels
                                                       linear
                                                       mRNA
                                                 615 bp
Sequence 3 from Patent WO0220754.
AX721043
                                                                                             AX721043.1 GI:30421879
                                                                                                                             Homo sapiens (human)
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                        RESULT 13
AX721043
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                          ORGANISM
                                                                                                                                                                                     REFERENCE
AUTHORS
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JOURNAL
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                                                                                                 PAT 03-FEB-2004
                                                                                                                                                                                                                                           Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462
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                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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40.1%; Score 577; DB 6; Length 577;
Best Local Similarity 100.0%; Pred. No. 2.9e-128;
Matches 577; Conservative 0; Mismatches 0; Indels
              721 TTTGGCGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGGCAG 763
                                                                                                 linear
TTTGGCGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGGCAG 979
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Patent: WO 02068579-A 10688 06-SEP-2002;
PR Corporation (NY) (US)
Location/Qualifiers
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                                                                                                 CQ724754 577 bp DNA
Sequence 10688 from Patent WO02068579.
CQ724754 GI:42285611
                                                                                                                                                                                                                                                                                                                                                 1. :577
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                       Homo sapiens (human)
937
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KRYWORDS
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                                                                                                                                                                                     ORGANISM
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AUTHORS
TITLE
                                                                     RESULT 12
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                                                                                                                                                                                                                                                                                                      JOURNAL
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VERSION KEYWORDS -SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

ACCESSION

RESULT 14 BC062516

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/product="hypothetical protein MGC76170"

/protein id="AAH62516.1"

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/brotein id="AAH62516.1"

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ILTEHLSSESSHGWYLLAPPRDTDQAALLKODAGFVPNRVFSLDLSDDVVIERLSLC
MDPVSGERYHDIXKPAPSSEVHERLQQNPRHSEQRYQARLDWYHANABELDEFYPDV
IHINDQDPYTVFRETESYTVSPLPRELPERFYSP"
/clone="MGC:76170 IMAGE:5335533"
(tissue_type="Embryo, Silurana tropicalis, tailbud (stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AACCACATCTTCGAGTTGATGCAGAACATGCTGGAGCAACTCCTGATCCACCAGCCCGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 CTGAACAGCAGTCTCCTCACCCTGGAGAACCTGATCTTAAATGAGTTTTCCTATACGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 553.8; DB 5;
Pred. No. 1.1e-122;
0; Mismatches 552;
                                                                                                                                                                                                                                /note="Vector: pCMV-SPORT6.1"
                                                                                                                                           'clone lib="NICHD XGC Emb7"
                                                                                                                                                                                                                                                                                                                 gene="MGC76170"
db_xref="LocusID:394708"
                                                                                                                                                                                   host="DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MGC76170"
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Best Local Similarity 61.6%;
Matches 885; Conservative (
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Klausherg, R.L., Feingold, E.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mullahy, S.J., Bossak, S.A., McEwah, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skaleka, U., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences

N. Paror, M. P. Proc. Nat. Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                           mRNA linear VRT 23-AUG-2004
protein MGC76170, mRNA (cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 142 Row: e Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-NOV-2003) National Institutes of Health, Xenopus (Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbe-remail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                    Xenopus tropicalis (Silurana tropicalis)
Xenopus tropicalis
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MGC:76170 IMAGE:5335533), complete cds.
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1 (bases 1 to 1674)
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Contact: XGC help desk
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961 TITGAAAAGGAGATGGCAGTTCCTGACAGCCTCCTCATGAAGGTGCTGAGGCCAGCGCCTG 1020
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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GAGTATCATAGGAACATCGTCAGGGTCATTCCCTCCTACCCCAAAATCCTCAAAGTCATC 720
                                                                                                                                                            666 GAGTACCACAGAAATATCCCAGGCATATTGCGCACTTACCCAAAGACGTCCAAGAAGATA 725
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 100.0%; Pred. No. 5.4e-66;
Matches 319; Conservative 0; Mismatches 0;
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| coganism="Mono sapiens" | /mol_type="unassigned DNA" | /db_xref="taxon:9606"
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